

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
27 December 2001 (27.12.2001)

PCT

(10) International Publication Number
WO 01/98526 A2

(51) International Patent Classification⁷: **C12Q**

(21) International Application Number: PCT/US01/20122

(22) International Filing Date: 22 June 2001 (22.06.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/213,812 22 June 2000 (22.06.2000) US
09/804,291 13 March 2001 (13.03.2001) US

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,
SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished
upon receipt of that report*

*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*



WO 01/98526 A2

(54) Title: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND BIOSENSORS OF CHEMICAL SENSANTS

(57) Abstract: The use of sensory G protein-coupled receptors that recognize chemical sensants, particularly those involving olfactory and taste receptors; polypeptide fragments and mutants thereof; classes of such receptors; polynucleotides encoding such receptors, fragments and mutants thereof, and representatives of receptor classes; genetic vectors including such polynucleotides; and cells and non-human organisms engineered to express such receptor complexes, fragments and mutants of an olfactory or taste receptor, and representatives of receptor classes to simulate sensory perception of odorants and tastants is described. The use of such products as a biosensor or a components thereof to detect, identify, measure, or otherwise process the event of binding between the receptor and its cognate ligand (*i.e.*, chemical sensant) is also described. The invention has application, for example, in the design and formulation of odorant and tastant compositions.

RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND BIOSENSORS OF CHEMICAL SENSANTS

5 Cross Reference to Related Application

This application is related to U.S. Provisional Serial No. 60/213,812, filed June 22, 2000, and U.S. Serial No. 09/804,291, filed March 13, 2001, which are incorporated by reference in their entirety.

10 **Background of the Invention**

Field of the Invention

The invention relates to the use of sensory G protein-coupled receptor complexes that recognize chemical sensants, particularly those involving olfactory and taste receptors; polypeptide fragments and mutants thereof; classes of such receptors; polynucleotides encoding such receptors, fragments and mutants thereof, and representatives of receptor classes; genetic vectors including such polynucleotides; and cells and non-human organisms engineered to express such receptor complexes, fragments and mutants of an olfactory or taste receptor, and representatives of receptor classes to simulate sensory perception of odorants and tastants. The invention also relates to the use of such products as a biosensor or component thereof to detect, to identify, to measure, or otherwise process the event of binding between the receptor and its cognate ligand (*i.e.*, chemical sensant). The invention has application, for example, in the design and formulation of odorant and tastant compositions.

25 Description of the Related Art

The olfactory and taste systems provide sensory information about the chemical environment. Olfactory receptors and taste receptors recognize, respectively, “odorants” and “tastants,” collectively referred to as “sensants” or “sensory receptor ligands” herein. A “primary” sensant is an odorant or tastant ligand that substantially binds to sensory receptors with a ligand-binding site of a single amino acid sequence. Olfactory and taste receptors belong to the superfamily of seven-transmembrane guanyl nucleotide-binding proteins: such receptors are, however, also recognized as distinct families, or sub-genuses, of olfactory or taste

receptors (see Raming *Nature* 361:353, 1993). These receptors control diverse physiological functions such as media-ting signaling from an external chemical stimulus across the membrane containing the receptor into a cell, endocrine function, exocrine function, heart rate, lipolysis, and carbohydrate metabolism. Thus, the
5 dissection of these diverse functions into component signals is needed.

But the complexities of sensory perception of chemical sensants prevent easy translation of the olfaction and taste systems to a machine sensor. For example, U.S. Patent Nos. 5,675,070; 5,918,257; 5,928,609; and 6,085,576 disclose machine sensors that use various chemistries, but they do not take advantage of the specificity of
10 olfactory and taste receptors for their cognate ligands to produce a biosensor.

WO 00/15269 discloses methods and apparatus for odor reproduction. The total affinities of a specific odorant with a group of receptors was called the affinity fingerprint of the odorant. This odorant fingerprint was represented by a vector of affinity values. It was proposed to repro-duce an arbitrary odor by inputting its sensed
15 odorant fingerprint into a device, which has a palate of predetermined odorants and produces a composite odor using predetermined odorant finger-prints by minimizing the difference between vectors representing the sensed odorant fingerprint and the predetermined odorant fingerprints. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

20 WO 00/70343 discloses biosensors and sense replication systems using G-protein coupled receptors (GPCR). It was proposed to mimic the response of the G-protein signal transduction system by detecting the affinity of a stimulus to a plurality of GPCR, codifying such information into electronic signals, and reproducing the stimulus by converting the codified information into a combination of stimulant
25 entities. But this reference also does not teach or suggest the human olfactory receptors disclosed herein.

WO 01/27158 discloses olfactory receptors and their use to determine the correspondence between individual odorant receptors and particular odors. It was proposed that the interactions between an odor and olfactory receptors can be used to
30 represent the odor and to re-create it. This reference, however, does not teach or suggest the human olfactory receptors disclosed herein.

Dissecting the function of sensory receptors by binding sensory receptors of a clone of cells expressing a single sensory receptor gene, fragmentation of sensory

receptors to provide ligand-binding or signal-transducing domains thereof, and construction of fusion sensory receptor proteins will separate the diverse physiological functions associated with sensory perception at the level of ligand-receptor binding. Furthermore, novel "primary sensants" that are identified and isolated by the methods described herein may be used to further define the function of the cognate sensory receptor by uniquely enhancing or, in the alternative, blocking stimulation of sensory receptors with a single ligand-binding domain.

The present invention addresses the need for better understanding of these ligand-receptor interactions by using a large set of identified sensory receptors. Even if the receptor set used is incomplete (*i.e.*, a partial set of all sensory receptors encoded in the genome), a large number of sensants will be detected. Moreover, redundancy in the chemical structures recognized by the sensory receptors or combinatorial processing of signals from different sensory receptors would allow broad coverage of chemically diverse sensants (*e.g.*, by selection of a representative class of sensory receptors). Also provided are, *inter alia*, methods for utilizing such sensory receptors and biosensors to simulate sensory perception. To analyze ligand-receptor interactions and their effects on cell signaling and the processing of those signals in sensory perception, specific sensants and their cognate receptor complexes are detected, identified, and measured under binding conditions. Fragrances and flavorings can be detected, identified, measured, and/or custom designed by the methods herein described. In addition, drugs that incorporate artificial odors and/or tastes can be formulated.

Summary of the Invention

Large gene families encoding mammalian olfactory G-protein-coupled receptors (OLFR) and mammalian taste G-protein-coupled receptors (TASR) are known in the prior art or are disclosed herein. An object of the invention to provide fragments and variants of such OLFRs and TASRs which retain odorant- or tastant-binding activity, respectively. The large number of sensory receptors that are made available herein and now amenable to manipulation raises the confidence that a substantially complete, or at least functional, repertoire of sensory receptors is provided.

It is an object of the invention to provide nucleic acid sequences or molecules that encode such sensory receptors, or fragments or variants thereof. Another object is to provide expression vectors which include nucleic acid sequences that encode such sensory receptors, or fragments or variants thereof. It is yet another object of the invention to provide human or non-human cells which functionally express at least one of such sensory receptors, or fragments or variants thereof. Still another object is to provide sensory receptor fusion proteins or other polypeptides which include at least a fragment of at least one of such sensory receptors. In particular, fusions with reporter molecules or other heterologous amino acid sequences may maintain the original ligand-properties while changing the signaling properties to allow easier detection of sensant binding to the receptor (*e.g.*, change in fluorescent signal). Moreover, chimeric proteins or other polypeptides with altered ligand-binding and/or signaling properties can be made from two or more different sensory receptors by mixing domains.

The invention provides methods for representing the sensory perception of one or more chemicals (*e.g.*, a primary sensant or mixture thereof) and/or for predicting the sensory perception of one or more chemicals in a mammal (*e.g.*, human) using the aforementioned products. Given a known member of a ligand-receptor binding pair, one or both members of the pair (*i.e.*, ligand, receptor, or both) may be detected, identified, and/or measured under binding conditions.

Novel molecules or combinations of molecules which elicit a desired and predetermined sensory perception in a mammal (*e.g.*, human) can be generated by determining a value of sensory perception in a mammal for a known molecule or combination thereof; determining a value of sensory perception in a mammal for one or more unknown molecules or combinations thereof; comparing the value of sensory perception in a mammal for one or more unknown compositions to the value of sensory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined sensory perception in a mammal; and mixing two or more unknown molecules or combinations thereof to form a molecule or combination thereof that elicits a predetermined sensory perception in a mammal. The combining step yields a single molecule or a combination thereof that elicits a predetermined sensory perception in a mammal. In particular, primary odorants that uniquely bind to olfactory receptors with a single

ligand-binding domain may be such novel molecules. Variants thereof may be used (1) to enhance stimulation of a limited response by olfactory receptors with a single ligand-binding domain or (2) to block stimulation of olfactory receptors with a single ligand-binding domain to reduce or inhibit olfactory perception. An alternative method for identifying primary odorants is to identify the mutated receptors in genetic anosmias because that odorant would be expected to be recognized by only one or a few olfactory receptors affected by the mutation.

Detailed Description of the Invention

10 Perception of Chemical Sensants

U.S. Patent No. 5,691,188 describes how upon binding of ligand to receptor, the receptor presumably undergoes a conformational change leading to activation of the G protein. The G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of disso-ciation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell. A high-resolution X-ray crystal structure is available for rhodopsin, a guanyl nucleotide binding protein, has been solved (Palczewski *et al.*, *Science* 289:739, 2000). Using this structure, the portions of the amino acid sequence of sensant receptors that are responsible for ligand binding can be identified.

30

Sensory Perception - Olfaction

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel *Sci. Amer.* 273:154, 1995). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer *Semin. Cell Biol.* 5:25, 1994). The human genome contains thousands of genes that encode a diverse repertoire of olfactory receptors (Rouquier *Nat. Genet.* 18:243, 1998; Trask *Hum. Mol. Genet.* 7:2007, 1998). An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that sensory receptors belong to a multigene family with over a thousand members, and the odorant receptors number at least 500 to 1,000. Moreover, each sensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses.

Sensory Perception - Taste

Mammals are believed to have five basic taste modalities: sweet, bitter, sour, salty, and umami (the taste of monosodium glutamate). See, e.g., Kawamura *et al.*, *Introduction to Umami: A Basic Taste* (1987); Kinnamon *et al.*, *Ann. Rev. Physiol.*, 54:715, 1992; Lindemann, *Physiol. Rev.*, 76:718, 1996; Stewart *et al.*, *Am. J. Physiol.*, 272:1, 1997. Numerous physiological studies in animals have shown that taste receptor cells may selectively respond to different chemical stimuli. See, e.g., Akabas *et al.*, *Science*, 242:1047, 1988; Gilbertson *et al.*, *J. Gen. Physiol.*, 100:803, 1992; Bernhardt *et al.*, *J. Physiol.*, 490:325, 1996; Cummings *et al.*, *J. Neurophysiol.*, 75:1256, 1996.

In mammals, taste receptor cells are assembled into taste buds that are distributed into different papillae in the tongue epithelium. Circumvallate papillae, found at the very back of the tongue, contain hundreds, e.g., mice, to thousands, e.g., human, of taste buds. By contrast, foliate papillae, localized to the posterior lateral edge of the tongue, only contain dozens to hundreds of taste buds. Moreover, fungiform papillae contain only a single or a few taste buds, and are at the front of the tongue.

AC010814, AC018700, AC021304, AC008620, AC011537, AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, 5 AP001803, AP001804, AL353767, AP001884, AC026083, AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, 10 AP002826, AL359636, AL391534, AC055731, AC076959, AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes. Similarly, genes encoding five and thirty-six (36) distinct, novel human T1R and T2R taste receptors, respectively, have been identified in genome 15 sequence databases.

Alternatively, nucleic acids encoding the sensory receptors and other related polypeptides can be isolated from a variety of sources, genetically engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 00/35374, which is herein incorporated by reference in its entirety.

20 These nucleic acids provide probes for the identification of cells expressing sensory receptors, as the nucleic acids are specifically expressed in such cells. They can also serve as tools for the generation of sensory topographical maps that elucidate the relationship between cells expressing sensory receptors and sensory neurons leading to particular regions of the brain. Furthermore, the nucleic acids and the 25 polypeptides they encode can be used as probes to elucidate olfactant- or tastant-induced behaviors.

Nucleic acid molecules encoding a sensory receptor comprising a nucleic acid sequence that is at least 75%, 85%, 90%, 95%, or 99% identical to a nucleic acid sequence selected from those known in the prior art or disclosed herein are considered 30 variants. Other nucleic acid molecules comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence at least 75%, 85%, 90%, 95%, or 99% identical to an amino acid sequence selected from those known in the prior art or disclosed herein are also considered variants. Further variants contain amino acid

sequence differences in at most ten, five, four, three, two, or one amino acid residue(s).

Exemplary nucleic acid sequences may be selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID

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 SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512.

Nucleic acid molecule comprising a nucleic acid sequence that encodes a
 fragment of a polypeptide having an amino acid sequence selected from those known
 in the prior art or disclosed herein; wherein the fragment is at least ten, 20, 30, 50, 70,
 30 100, or 150 amino acid residues in length, are useful as probes, primers, and to
 construct hybrids or chimerae.

Polypeptides comprising an amino acid sequence that is at least 90%, 95%,
 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from those

known in the prior art or disclosed herein are considered variants. Further variants contain amino acid sequence differences in at most ten, five, four, three, two, or one amino acid residue(s). Other polypeptides comprising a fragment of a polypeptide having an amino acid sequence selected from those known in the prior art or disclosed
5 herein; wherein the fragment is at least 40, 60, 80, 100, 150, 200, or 250 amino acid residues in length, are useful as specific binders of sensants, competitive binders, antigens, and to construct hybrids or chimerae.

Exemplary amino acid sequences may be selected from the group consisting of
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NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,
SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID
20 NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,
SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID
NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,
SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID
NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,
25 SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID
NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,
SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID
NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,
SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID
30 NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Also provided are methods of screening for modulators, *e.g.*, activators,
inhibitors, stimu-lators, enhancers, agonists, and antagonists, of the sensory receptors,

or fragments or variants thereof. Such modulators of signal transduction are useful for pharmacological or genetic modulation of signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of sensory cell activity. These modulator compounds can then be used in the pharmaceutical, food, and cosmetic industries to customize odorants or tastants.

Thus, the invention provides assays for sensory modulation, where the sensory receptors, or fragments or variants thereof, act as direct or indirect reporter molecules for the effect of modulators on signal transduction. Sensory receptors, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo*, and *ex vivo*. In one embodiment, sensory receptors, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.*, Mistili *et al.*, *Nature Biotech.*, 15:961, 1997). In another embodiment, the sensory receptors, or fragments or variants thereof, can be expressed in host cells, and modulation of signal transduction via sensory receptor activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of signal transduction include *in vitro* ligand binding assays using the sensory receptors, or fragments or variants thereof. More particularly, such assays can use the sensory receptors; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G-protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting sensory receptor nucleic acid and protein expression, allowing for the investigation of taste transduction regulation and specific identification of sensory receptor cells. The sensory receptors, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying a sensory receptor cells. Sensory receptor cells can be identified using techniques such as reverse transcription and amplification

of mRNA, isolation of total RNA or poly A⁺ RNA, Northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, Western blots, and the like.

A. Identification and Characterization of Sensory Receptors

5 The amino acid sequences of the sensory receptors and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

10 For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as
15 described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

 A "comparison window," as used herein, includes reference to a segment of
20 any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment
25 of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970, by the search for similarity method of Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and
30 TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J Mol. Biol.* 215:403, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J. Mol. Biol.* 215:403, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (see, e.g., Figure 2). PILEUP uses a simplification of the progressive

alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351, 1987. The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151, 1989. The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the

5 pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by

10 designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can

15 be obtained from the GCG sequence analysis software package, *e.g.*, version 7. 0 (Devereaux *et al.*, *Nucl. Acids Res.* 12:387, 1984) encoded by the genes were derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian

20 olfactory receptor family, each of the olfactory receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative sensory receptor proteins generally having lengths of about 300 to

25 about 400 amino acid residues that contain seven transmembrane domains, as predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the 256 sensory receptors identified herein has a characteristic sequence signature of an olfactory

30 receptor. In particular, all 256 sequences contain very close matches to the following consensus amino acid motifs (Mombaerts, 1999; Pilpel, 1999): LHTPMY in intracellular loop 1, MAYDRYVAIC at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5,

FSTCSSH in the beginning of transmembrane domain 6, and PMLNPF in transmembrane domain 7. Combination of all the above mentioned structural features of the 256 genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

5 As noted above, complete or partial sequences of numerous human and other eukaryotic sensory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human sensory receptors, which suggests their different specificity in sensant recognition. Therefore, these novel sensory receptors and their genes can be used, alone or in combination
10 with known sensory receptors, in developing detection systems and assays for chemically distinct types of sensants not recognized by the known sensory receptors, as well as for diagnostic and research purposes.

B. Definitions

The terms "purified," "substantially purified," and "isolated" as used herein
15 refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the
20 compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or
25 concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or
30 proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

The terms “amplifying” and “amplification” refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, sensant-binding sequences of the invention) *in vivo* or *in vitro*.

The term “7- transmembrane receptor” means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma membrane seven times (thus, the seven domains are called “transmembrane” or “TM” domains TM I to TM VII). The families of olfactory and taste receptors each belong to this super-family. Seven-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

The term “expression vector” refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, *i.e.*, drive only transient expression in a cell. The term includes recombinant expression “cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

The term “library” means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated sensory, particularly olfactory or taste, receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of vectors that incorporate the amplified sensant-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding a sensory receptor.

The term “nucleic acid” or “nucleic acid sequence” refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, *i.e.*, oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like

structures with synthetic backbones, *see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Anti-sense Strategies*, Annals of the N.Y. Academy of Sciences, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan (1993) *J. Med. Chem.* 36:1923-1937; *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata (1997) *Toxicol. Appl. Pharmacol.* 144:189-197; Strauss-Soukup (1997) *Biochemistry* 36:8692-8698; Samstag (1996) *Antisense Nucleic Acid Drug Dev* 6:153-156.

The term sensory receptor "ligand-binding region" refers to sequences derived from a sensory receptor that substantially incorporates transmembrane domains II to VII (TM II to VII). The domain may be capable of binding a sensant.

The terms "conservative variant" or "analog" or "mimetic" refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the poly-peptide's (the conservative variant's) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, etc.) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing function-ally similar amino acids are well known in the art.

For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): Ala/Gly or Ser; Arg/Lys; Asn/Gln or His; Asp/Glu; Cys/Ser; Gln/Asn; Gly/Asp; Gly/Ala or Pro; His/Asn or Gln; Ile/Leu or Val; Leu/Ile or val; Lys/Arg or Gln or Glu; Met/Leu or Tyr or Ile; Phe/Met or Leu or Tyr; Ser/Thr; Thr/Ser; Trp/Tyr; Tyr/Trp or Phe; Val/Ile or Leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g., Creighton, Proteins*, W.H. Freeman, 1984; Schultz & Schimer, *Principles of Protein Structure*, Springer-Verlag, 1979). One of skill in the art will appreciate that the above-identified substitutions are not the only possible

conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains or sensant-binding domains or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity. As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (see, *e.g.*, Spatola (1983) in *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. 7, pp 267-357, "Peptide Backbone Modifications,"

Marcell Dekker, NY). A polypeptide can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, e.g., inducible or constitutive expression of a fusion protein comprising a translocation domain of the invention and a nucleic acid sequence amplified using a primer of the invention.

The term "transmembrane domain" means a polypeptide domain that can completely span the plasma membrane. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below.

C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the sensory receptors, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (e.g., promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature. See, *e.g.*, Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I, Theory and Nucleic Acid Preparation*, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, *e.g.*, analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, *e.g.*, fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), immunofluorescent assay, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (*e.g.*, SDS-PAGE),

RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (*PCR Protocols, a Guide to Methods and Applications*, ed. Innis. Academic Press, NY, 1990 and *PCR Strategies*, ed. Innis, Academic Press, NY, 1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560, 1989; Landegren, *Science* 241:1077, 1988; Barringer, *Gene* 89:117, 1990); transcription amplification (see, e.g., Kwoh, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989); and, self-sustained sequence replication (see, e.g., Guatelli, *Proc. Natl. Acad. Sci. USA* 87:1874, 1990); Q Beta replicase amplification (see, e.g., Smith, *J. Clin. Microbiol.* 35:1477, 1997); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257, 1996) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307, 1987; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563, 1995.

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, e.g., U.S. Patent No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the sensant-binding region-coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted sensant-binding domain comprises substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I

and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify sensant-binding regions of olfactory receptor proteins. These domain regions may vary for different sensants, and more particularly odorants; thus, what may be a minimal binding region for one sensant, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane sensory receptor.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL. Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII.

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3'). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify a transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL, encoded by a sequence such as 5'-

AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CA-NGT-3'. Such a degenerate primer can
5 be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and
10 is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g., Rose, Nucl. Acids Res.* 26:1628, 1998; Singh, *Biotechniques* 24:318, 1998).

Means to synthesize oligonucleotide primer pairs are well known in the art.
15 "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition.
20 Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866, 1997. Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950, 1998). For example, two degenerate bases can
25 be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, Proc. Natl. Acad. Sci. USA* 95:4258, 1998). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-
30 cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, *see above*). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' and
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.

Nucleic acids that encode ligand-binding regions of olfactory receptors are generated by amplification (*e.g.*, PCR) of appropriate nucleic acid sequences using degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova, *Proc. Natl. Acad. Sci. USA* 93:9858, 1996). Shirley, *Eur. J. Biochem.* 32:485, 1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211, 1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*,

antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260, 1999), describes differentiated olfactory receptor-expressing cells in culture that respond to odorants, as measured by an influx of calcium.

5 Hybrid protein-coding sequences comprising nucleic acids sensory receptors fused to the translocation sequences described herein may be constructed. Also provided are hybrid receptors comprising the translocation motifs and ligand-binding domains of sensory receptors. These nucleic acid sequences can be operably linked to transcriptional or translational control elements, *e.g.*, transcription and translation
10 initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can
15 also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227, 1998). Receptor genes are normally expressed in a small subset of
20 neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

 Fusion proteins, either having C-terminal or, more preferably, N-terminal
25 translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized
30 metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289, 1998), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615, 1997); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane
5 expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a nucleic acid sequence encoding a polypeptide linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787, 1995), and an amino terminal translocation domain. The histidine residues facilitate detection and
10 purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, *see, e.g., Kroll, DNA Cell. Biol.* 12:441, 1993).

Expression vectors, either as individual expression vectors or as libraries of
15 expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent literature. *See, e.g., Roberts, Nature* 328:731, 1987; Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10, 1995; Sambrook; Tijssen; Ausubel. Product information from
20 manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses
25 which are stably or transiently expressed in cells (*e.g., episomal expression systems*). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic
30 resistance (*e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin*) or herbicide resistance (*e.g., chlorosulfuron or Basta*) to permit selection of those cells transformed with the desired DNA sequences (*see, e.g., Blondelet-Rouault, Gene* 190:315, 1997; Aubrecht, *J. Pharmacol. Exp. Ther.* 281:992, 1997). Because

selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

A chimeric nucleic acid sequence may encode a sensant-binding domain within any 7-transmembrane polypeptide. Seven-transmembrane receptors belong to a superfamily of trans-membrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-trans-membrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (e.g., TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969, 1999; Rost, *Protein Sci.* 4:521, 1995. Periodicity detection enhancement and alpha helical periodicity index can be done as by, e.g., Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, see, e.g., Peitsch, *Receptors Channels* 4:161, 1996; Cronet, *Protein Eng.* 6:59, (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, e.g., TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (e.g., PCR) from mRNA of or cDNA derived from, e.g., olfactory receptor-expressing neurons or genomic DNA.

Libraries of sensory receptor ligand-binding TM domain sequences can include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, e.g., homology modeling, Fourier analysis and helical periodicity (see, e.g., Pilpel *supra*), as described above. Using this information sequences flanking the seven

domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,
5 for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the sensory receptors described herein, coupled to additional amino acids representing all or part of another
10 G protein receptor, preferably a member of the 7-transmembrane superfamily. These chimerae can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the 7-transmembrane protein described herein, and the
15 remaining portion or portions come from another G protein-coupled receptor.

Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled in the art can readily be used to create such chimeric receptors. The use of such
20 chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand binding domain, an extracellular
25 domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous CGPCR
30 extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, e.g., green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to a sensory receptor disclosed herein can be isolated using the nucleic acid probes described above. Alternatively, expression libraries can be used to isolate sensory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against a sensory receptor-derived polypeptide, which also recognize and selectively bind to the sensory receptor homolog.

Also within the scope of the invention are host cells for expressing the sensory receptors, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the sensory receptors, fragments, or variants thereof, the nucleic acid sequence of interest is subcloned into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable prokaryotic and eukaryotic expression systems are well known in the art and described, e.g., in Sambrook *et al.*

Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasmid vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g., Sambrook et al.*). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.,* WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of Sensory Receptor Polypeptides

In addition to the detection of sensory receptor genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect

sensory receptors, *e.g.*, to identify olfactory receptor cells, and variants of sensory receptor family members. Immunoassays can be used to qualitatively or quantitatively analyze the sensory receptors. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

5 1. Antibodies to sensory receptor family members

Methods of producing polyclonal and monoclonal antibodies that react specifically with a sensory receptor family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology*, 1991; Goding, *Monoclonal Antibodies: Principles and Practice*, 2d ed., 1986; Harlow & Lane, *supra*; and Kohler & Milstein, *Nature*, 256:495, 1975). Such techniques include antibody preparation by
10 selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (*see, e.g.*, Huse *et al.*, *Science*, 246:1275, 1989; Ward *et al.*, *Nature*, 341:544, 1989).

15 A number of sensory receptor-comprising immunogens may be used to produce antibody specifically reactive with a sensory receptor family member. For example, a recombinant sensory receptor protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the sensory receptor family.
20 Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used an immunogen. Naturally occurring
25 protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in
30 the art. Mice, hamsters, rats, guinea pigs, rabbits, goats, or chickens is immunized with the protein using an adjuvant (*e.g.*, Freund's adjuvant) and a standard immunization protocol with periodic boosts. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of

reactivity to the sensory receptor. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (see Harlow & Lane, *supra*).

5 Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen are immortalized, commonly by fusion with a myeloma cell (see Kohler & Milstein, *Eur. J. Immunol.*, 6:511, 1976). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, retroviruses, or other
10 methods well known in the art. Colonies arising from single clones of immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a
15 monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275, 1989.

 Monoclonal antibodies or polyclonal sera are collected and titered against antigen in an immunoassay, for example, a solid phase immunoassay with the antigen
20 immobilized on a solid support. Typically, polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against non-sensory receptor proteins, or even other sensory receptor family members or other related proteins from other organisms, using a competitive binding immuno-assay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1
25 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

 Once sensory receptor family member specific antibodies are available, individual sensory receptor proteins can be detected by a variety of immunoassay methods. For a review of immuno-nological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed., 1991). Moreover, the
30 immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

2. Immunological binding assays

Sensory receptor proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patent Nos. 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general
5 immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed., 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case a sensory receptor family member or an antigenic subsequence thereof). The antibody (e.g., anti-sensory
10 receptor) may be produced by any of a number of means well known to those of skill in the art and as described above.

Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent
15 may be a labeled sensory receptor polypeptide or a labeled anti-sensory receptor antibody. Alternatively, the labeling agent may be a third moiety, such a secondary antibody, that specifically binds to the antibody/sensory receptor complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding
20 immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g., Kronval et al., J. Immunol.*, 111:1401, 1973; Akerstrom *et al., J. Immunol.*, 135:2589, 1985). The labeling agent can be modified with a detectable moiety, such as biotin, to which
25 another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the
30 incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting a sensory receptor protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays directly measure the amount of antigen. In one preferred "sandwich" assay, for example, the anti-sensory receptor antibodies are bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the sensory receptor protein present in the test sample. The sensory receptor protein thus immobilized is then bound by a labeling agent, such as a second anti-sensory receptor antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g.*, streptavidin, to provide a detectable moiety.

b. Competitive assay formats

In competitive assays, the amount of sensory receptor protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) sensory receptor protein displaced (competed away) from an anti-sensory receptor antibody by the unknown sensory receptor protein present in a sample. In one competitive assay, a known amount of sensory receptor protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the sensory receptor. The amount of exogenous sensory receptor protein bound to the antibody is inversely proportional to the concentration of sensory receptor protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of sensory receptor protein bound to the antibody may be determined either by measuring the amount of sensory receptor protein present in a sensory receptor/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of sensory receptor protein may be detected by providing a labeled sensory receptor molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known sensory receptor protein is immobilized on a solid substrate. A known amount of anti-sensory receptor antibody is added to the sample, and the sample is then contacted with the immobilized sensory receptor. The amount of anti-sensory receptor antibody bound to the known immobilized sensory receptor protein is

inversely proportional to the amount of sensory receptor protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the
5 subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the
10 nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (e.g., sensory receptor proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the sensory receptor polypeptide encoded by the nucleic
15 acid sequences disclosed herein to compete with itself. The percentage cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins,
20 e.g., distantly related homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the sensory receptor family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be
25 perhaps an allele or polymorphic variant of a sensory receptor family member, to the immunogen protein (i.e., sensory receptor protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is
30 determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to

specifically bind to the polyclonal antibodies generated to a sensory receptor immunogen.

Antibodies raised against sensory receptor conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the sensory receptor family, but not to GPCRs from other families. Polyclonal antibodies that specifically bind to a particular member of the sensory receptor family, can be make by subtracting out cross-reactive antibodies using other sensory receptor family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human T2R01 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OLFR1 or mouse OLFR1.

d. Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of sensory receptor protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the sensory receptor protein. The anti-sensory receptor polypeptide antibodies specifically bind to the sensory receptor poly-peptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-sensory receptor antibodies.

Other assay formats include liposome immunoassays (LIA) using liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34, 1986).

e. Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immo-bilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein

compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

f. Labels

The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immuno-assays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, bio-chemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADS™, fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., ^3H , ^{125}I , ^{35}S , ^{14}C , or ^{32}P), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, etc.).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to another molecules (e.g., streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a sensory receptor protein, or secondary antibodies that recognize anti-sensory receptor.

The molecules can also be conjugated directly to signal generating compounds, e.g., by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone,

etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, see U.S. Patent No. 4,391,904.

Methods for detecting labels are well known. Thus, for example, where the label is a radioactive label, it may be detected using a scintillation counter or with photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluoro-chrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, with photographic film, or using electronic detectors such as charge coupled devices (CCDs) or photomultipliers. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian sensory, and more particularly, olfactory receptor of the invention, both *in vitro* and *in vivo* are described below, as are methods and compositions for determining whether a test compound is neurotoxic to an olfactory neuron expressing an olfactory transmembrane receptor polypeptide. Any aspect of cell physiology can be monitored to assess the effect of sensant-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical

stimuli into electrical signals. An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G-proteins, and modulation of diverse channels by Gi and other G-proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The sensory receptor protein of the assay will typically be selected from a natural poly-peptide or conservatively modified variant thereof. Generally, the amino acid sequence identity will be at least 75%, 85%, 90%, 95%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of a sensory receptor protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand binding domain, subunit association domain, active site, and the like. Either the sensory receptor protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein.

Modulators of sensory receptor activity can be tested using sensory receptor polypeptides as described above, either recombinant or naturally occurring. Protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. In vitro binding assays

Sensory perception can also be examined *in vitro* with soluble or solid state reactions, using a full-length sensory receptor-GPCR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a sensory receptor covalently linked to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of a sensory receptor. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises all or part of a sensory receptor polypeptide, as well an additional sequence that facilitates the localization of the

sensory receptor to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein.

Ligand binding to a sensory receptor protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties. Sensory receptors with large (*e.g.*, approximately 600 amino acid residues) extracellular N-terminal segments. These N-terminal segments are thought to form ligand-binding domains, and are therefore useful in biochemical assays to identify sensory receptor agonists and antagonists. Similar assays have been used with other GPCRs, such as the metabo-tropic glutamate receptors (*e.g.*, Han & Hampson, *J. Biol. Chem.* 274:10008, 1999). These assays might involve displacing a radioactively or fluorescently labeled ligand, and measuring changes in intrinsic fluorescence or changes in proteolytic susceptibility, *etc.*

Receptor-G-protein interactions can also be examined. For example, binding of the G-protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor sensant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation, or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the sensory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nano-seconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the sensory receptors of the invention, fluorescence-labeled sensants or auto-fluorescent sensants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where \parallel is the intensity of the emission light parallel to the excitation light plane and \perp is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For

example, the Beacon® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley *J. Anal. Toxicol.* 5, 236, 1981 which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$\text{Rotational Relaxation Time} = \frac{3\eta V}{RT}$$

The rotational relaxation time is small (≈ 1 nanosecond) for small molecules (*e.g.*, fluorescein) and large (≈ 100 nanoseconds) for large molecules (*e.g.*, immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Soluble and solid state high throughput assays

In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, *etc.*; a domain that is covalently linked to a heterologous protein to create a chimeric molecule; a sensory receptor protein; or a cell or tissue expressing a sensory receptor protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based *in vitro* assays in a high throughput format, where the domain, chimeric molecule, sensory receptor protein, or cell or tissue expressing the sensory receptor is attached to a solid phase substrate.

In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the taste transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,

describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

5 Yet another assay for compounds that modulate sensory receptor protein activity involves computer assisted drug design, in which a digital or analog processing system is used to generate a three-dimensional structure of a sensory receptor protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a
10 preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, *e.g.*, ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering
15 protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a sensory receptor polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of those described herein, or fragments or variants thereof.

20 The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*,
25 magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art.

The amino acid sequence represents a primary structure that encodes the
30 information necessary to form the secondary, tertiary and quaternary structure of the protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent

accessible surfaces, and hydrogen bonding. Secondary energy terms include van der Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the sensory receptor protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of sensory receptor genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used to identify patients having such mutated genes. Identification of the mutated sensory receptor genes involves receiving input of a first nucleic acid or amino acid sequence of a sensory receptor gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once

odorant dependent activation monitored. Control samples (untreated with activators or inhibitors) are assigned a relative sensory receptor activity value of 100. Inhibition of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of
5 a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electri-cal potential) of the cell or membrane expressing a sensory receptor protein. One means to deter-mine changes in cellular polarization is by measuring
10 changes in current, and thereby measuring changes in polarization, with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575, 1997). Whole cell currents are conveniently determined using the standard. Other known assays include: assays to measure ion flux using radiolabeled or fluorescent
15 probes such as voltage-sensitive dyes (*see, e.g.*, Vestergarrd-Bogind *et al.*, *J. Membrane Biol.*, 88:67, 1988; Gonzales & Tsien, *Chem. Biol.*, 4:269, 1997; Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185, 1991; Holevinsky *et al.*, *J. Membrane Biology*, 137:59, 1994). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

20 The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a
25 variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, Northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP3, cGMP, or cAMP.

Preferred assays for G-protein coupled receptors include cells that are loaded
30 with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G-protein coupled receptors as negative or positive controls to assess activity of tested compounds. In assays for identifying modulatory compounds (*e.g.*, agonists,

antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed in the Molecular Probes 1997 Catalog. For G-protein
5 coupled receptors, promiscuous G-proteins such as G α 15 and G α 16 can be used in the assay of choice (Wilkie *et al.*, *Proc. Natl. Acad. Sci.*, 88:10049, 1991). Such promiscuous G-proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*, increases in second messengers such as IP₃, which releases intracellular stores of
10 calcium ions. Activation of some G-protein coupled receptors stimulates the formation of inositol triphosphate (IP₃) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature* 312:315, 1984). IP₃ in turn stimulates the release of intracellular calcium ion stores. Thus, a change in cytoplasmic calcium ion levels, or a change in second messenger levels such as IP₃
15 can be used to assess G-protein coupled receptor function. Cells expressing such G-protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to
20 distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and
25 olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (see, *e.g.*, Altenhofen *et al.*, *Proc. Natl. Acad. Sci.*, 88:9868, 1991 and Dhallan *et al.*, *Nature* 347:184, 1990). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior
30 to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*, certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors,

serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, sensory receptor protein activity is measured by expressing a sensory receptor gene in a heterologous cell with a promiscuous G-protein that links the receptor to a phospholipase C signal transduction pathway (see Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995). Optionally the cell line is HEK-293 (which does not naturally express sensory receptor genes) and the promiscuous G-protein is Gal 5 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by measuring changes in intracellular Ca^{2+} levels, which change in response to modulation of the sensory receptor signal transduction pathway via administration of a molecule that associates with a sensory receptor protein. Changes in Ca^{2+} levels are optionally measured using fluorescent Ca^{2+} indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be measured using immunoassays. The method described in Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995, may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159, 1994, may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent No. 4,115,538, herein incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent No. 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing a sensory receptor protein of interest is contacted with a test compound for a sufficient time to

effect any interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent No. 5,436,128, herein incorporated by reference. The reporter genes can be, *e.g.*, chloramphenicol acetyltransferase, luciferase, β -galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (see, *e.g.*, Mistili & Spector, *Nature Biotech.* 15:961, 1997).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the sensory receptor protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the sensory receptor protein of interest.

6. Transgenic non-human animals expressing sensory receptors

Non-human animals expressing one or more sensory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of translocation domains in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize

odorants/ligands that can bind to a specific or sets of receptors. Such vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

- 5 Means to infect/express the nucleic acids and vectors, either individually or as libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses.
- 10 When electrodes are located on the olfactory bulb surface it is possible to record stable responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287, 1997). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of
- 15 one turbinate bone or were placed in corresponding positions on four turbinate bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950, 1997; Scott, *J. Neurophysiol.* 75:2036, 1996; Ezech, *J. Neurophysiol.* 73:2207, 1995. In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and
- 20 medial surface of the turbinates (*see, e.g.*, Youngentob, *J. Neurophysiol.* 73:387, 1995). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1, 1991).

- The sensory receptor sequences of the invention can be for example expressed
- 25 in animal nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *Proc. Natl. Acad. Sci. USA* 96:4040, 1999.

- The endogenous olfactory receptor genes can remain functional and wild-type
- 30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or
5 completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97, 1997). The insertion of the exogenous is typically by
10 homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotential embryonic stem (ES) cells
15 allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53, 1998); Moreadith, *J. Mol. Med.* 75:208, 1997; Tojo, *Cytotechnology* 19:161, 1995; Mudgett, *Methods Mol. Biol.* 48:167, 1995; Longo, *Transgenic Res.* 6:321, 1997; U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992;
20 5,627,059; 5,272,071; WO 91/09955; WO93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries can also be used as reagents to produce "knockout" human cells and their progeny.

F. Modulators

25 The compounds tested as modulators of a sensory receptor family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of a sensory receptor gene. Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential
30 modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by

automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (*e.g.*, in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO),
5 Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such
10 “combinatorial chemical libraries” or “ligand libraries” are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional “lead compounds” or can themselves be used as potential or actual therapeutics.

15 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical “building blocks” such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a
20 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not
25 limited to, peptide libraries (see, *e.g.*, U.S. Patent No. 5,010,175; Furka, *Int. J. Pept. Prot. Res.* 37:487, 1991; and Houghton *et al.*, *Nature* 354:84, 1991). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, WO 91/19735), encoded peptides (*e.g.*, WO 93/20242), random bio-oligomers (*e.g.*, WO 92/00091),
30 benzodiazepines (*e.g.*, U.S. Patent No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci.* 90:6909, 1993), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568, 1992), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer.*

Moreover, a method is provided for simulating a fragrance or flavor sensed by a mammal (*e.g.*, human), comprising: for each of a plurality of sensory receptors, or fragments or variants thereof, ascertaining the extent to which the sensory receptor interacts with the fragrance and/or flavor; and combining a plurality of compounds, each having a previously-determined interaction with one or more of the sensory receptors, in amounts that together provide a stimulation profile that mimics the profile for the fragrance and/or flavor. Interaction of a fragrance and/or flavor with a sensory receptor can be determined using any of the binding or reporter assays described herein. The interactions can be aggregated or a profile generated using known signal processing techniques (*e.g.*, a neural network) as described below. The sensory receptor, or fragments or variants thereof (*e.g.*, fusion proteins with reporters, chimeric proteins) may be expressed in cells; otherwise, ligand-binding domain(s) may be fixed to a substrate (*e.g.*, planar, bead, or fiber) that is solid or porous. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80%, 90%, 95%, 99% or all of the receptors that are substantially stimulated by the fragrance or flavor.

In yet another aspect of the invention, a method is provided in which a plurality of standard compounds are tested against a plurality of sensory receptors, or fragments or variants thereof, to ascertain the extent to which the sensory receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on data storage medium. The method may further comprise providing a desired receptor-stimulation profile for an odor and/or taste; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the odor and/or taste.

A further aspect of the invention is to provide a method for representing sensory perception of a particular odor and/or taste in a mammal (*e.g.*, human), comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is

greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; and generating from the values a quantitative representation of sensory perception. The sensory receptors may be a receptor disclosed herein, or fragments or variants thereof. The representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, or may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced sensory receptors, or fragments or variants thereof, with a composition and quantitatively measuring the interaction of the composition with the receptors. The maximum number of taste receptors that are needed to mimic the native repertoire (e.g., about 50) may be less than the maximum number of olfactory receptors that are needed (e.g., about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

It is yet another aspect of the invention to provide a method for predicting the sensory perception in a mammal (e.g., human) generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in the mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding known sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is

greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal by comparing the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal to the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal. The sensory receptors used in this method may include a receptor disclosed herein, or fragment or variant thereof. The maximum number of taste receptors that are needed to mimic the native repertoire (*e.g.*, about 50) may be less than the maximum number of olfactory receptors that are needed (*e.g.*, about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

Assaying for ligand-receptor binding in a large set of sensory receptors is envisioned to mimic the function of the nose or tongue in sensory perception of chemical sensants. For a set of sensory receptors with a redundancy of ligand-binding domains, the resultant signal is a summation of the interactions of all sensory receptors in the set: none, one, or a few of which have ligand-binding domains that are a perfect fit for the sensant; some of which have ligand-binding domains that are only an imperfect fit for the sensant; and most of which do not significantly bind to the sensant. The individual sensory receptor's binding affinity for sensant varies accordingly. Thus, a suitably large set of ligand-binding domains from sensory receptors will be analogous to any ability of the native repertoire of olfactory or taste receptors to tolerate varying degrees of mismatch between ligand and ligand-binding domain.

The complication of desensitization of sensory receptor signaling will also be avoided by using the invention instead of preparations of nasal or tongue epithelium containing native sensory receptors. For example, the event of binding between ligand and receptor can be separated from more complicated downstream signaling events in the epithelial cells. But the latter events can be reconstituted in the invention by transferring the sensory receptor of interest into appropriate host cells containing an intact and functional signaling pathway.

H. Administration of Novel Sensant Compositions

Sensory modulators can be administered directly to a mammal (*e.g.*, human) for modulation of sensory perception *in vivo*. Administration is by any of the routes normally used for introducing a modulator compound into ultimate contact with the tissue to be treated (*e.g.*, nose or tongue). The olfactory modulators are administered in any suitable manner, optionally with acceptable carriers. Suitable methods of administering such modulators are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route. Acceptable carriers are determined at least in part by the particular components of the composition to be administered (*e.g.*, stabilizing the sensants), as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present invention (*see, e.g., Remington's Pharmaceutical Sciences*, 17th ed. 1985).

The sensory modulators, alone or in combination with other suitable components, can be made into aerosol formulations (*i.e.*, they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichloro-difluoromethane, propane, nitrogen, and the like that may or may not contribute to sensory perception. Other possible formulation include dry or liquid forms, powders or tablets, solutions of polar (*e.g.*, water) or nonpolar (*e.g.*, alcohol) solvents, emulsions or suspensions, creams, gels, lotions, and syrups.

Formulations suitable for administration include aqueous and non-aqueous solutions, isotonic sterile solutions, which can contain antioxidants; buffers,

bacteriostats, and solutes that render the formulation isotonic, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. In the practice of this invention, compositions can be administered, for example, by orally, topically, intravenously, intraperitoneally, intravesically, or intrathecally. Optionally, the compositions are administered orally or nasally. The formulations of compounds can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials. Solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described. The modulators can also be administered as part of prepared drug, food, or cosmetic. In particular, an unpleasant odor or taste (*e.g.*, sulfur or bitter, respectively) may not be perceived as such and/or its effects reduced by blocking the binding between sensant ligand and sensory receptor by adding a competitor ligand that blocks binding between cognate ligand and receptor, or inhibiting or reducing signal transduction. In contrast, a pleasant odor or taste can be mimicked or enhanced. Primary sensants are preferred because the subset of activated cells is kept small and the effects limited to projection into a specific region of the brain. But novel olfactants or combinations thereof that bind only a few olfactory receptors (*e.g.*, having less than five different ligand-binding domains) would also be useful.

The dose administered to a mammal (*e.g.*, human) should be sufficient to effect a beneficial response in the subject over time. The dose will be determined by the efficacy of the particular sensory modulators employed and the condition of the subject, as well as the body weight or surface area of the area to be treated. The size of the dose also will be determined by the existence, nature, and extent of any adverse side-effects that accompany the administration of a particular compound or vector in a particular subject. In determining the effective amount of the modulator to be administered in a physician may evaluate circulating plasma levels of the sensory modulator, modulator toxicities, and the production of anti-modulator antibodies. In general, the dose equivalent of a modulator is from about 1 ng/kg to 10 mg/kg for the typical mammal. For administration, sensory modulators can be administered at a rate determined by the ED₅₀ of the modulator, and the side-effects of the inhibitor at various concentrations, as applied to the mass and overall health of the mammal. Administration can be accomplished via single or divided doses.

I. Kits

Sensory receptor genes, or fragments or variants thereof are useful tools for identifying cells expressing sensory receptors, for forensics and paternity determinations, and for examining signal transduction in isolated cells. Sensory
5 receptor family member-specific reagents that specifically hybridize to sensory receptor nucleic acids, such as AOFLF1 probes and primers, and sensory receptor specific reagents that specifically bind to a sensory receptor protein, *e.g.*, anti-sensory receptor antibodies are used to examine expression in cells and regulation of signal trans-duction. For example, one or more family member-specific reagents may be
10 used to detect poly-morphisms that are linked to genetic anosmia or to detect allelic exclusion.

Nucleic acid assays for the presence of DNA and RNA for a sensory receptor family member in a sample include numerous techniques are known to those skilled in the art, such as Southern analysis, Northern analysis, dot blots, RNase protection, S1
15 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such as to be available for hybrid-ization within the cell while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*,
20 *Biotechniques*, 4:230-250 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, a sensory receptor protein can be detected with the various immunoassay techniques described above. The test sample is typically compared to both a positive control (*e.g.*, a sample expressing a recombinant sensory
25 receptor protein) and a negative control.

The present invention also provides for kits for screening for novel modulators of sensory receptor family members. Such kits can be prepared from readily available materials and reagents, as well as any of the aforementioned products. For example, such kits can comprise any one or more of the following materials: sensory receptor
30 nucleic acids or proteins, reaction tubes, and instructions for testing sensory receptor activity. Optionally, the kit contains a biologically active sensory receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

Examples

AOLFR1 sequences:

- MKTFSSFLQIGRNMHQGNQTTITEFILLGFFKQDEHQNLLFVLFLGMYLVTVIGNGLIIV AISLD
 TYLHTPMYFLANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLLGTM
 5 AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIALHTLLLIQLLFCNHNTLPHFFCDLAPLL
 KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGWKAFSTCGSHLTVVLLFY
 GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTMPINPFYSLRNKDMKGALRKLINRKISSL (SEQ ID
 NO: 1)
- 10 ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
 CCATCACTGAATTCATTCTCCTGGGATTTTTCAAGCAGGATGAGCATCAAAAACCTCCTCTTT
 GTGCTTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA
 TCAGCTTGGATACGTACCTTCATACCCCCATGTATCTCTCCTTGCCAATCTATCCTTTGCT
 GATATTTCTCCATTTCCAACCTCAGTCCCCAAATGCTGGTGAATATTCAAACCAAGAGTC
 15 AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGCGTCATT
 GACAATTTGCTCTTGGGGACCATGGCCTATGACCACTTTGTGGCGATCTGCCACCCTCTGA
 ATTATACAATTCTCATGCGGCCAGGTTCCGGCATTGCTCACAGTCATCTCATGGTTCCTC
 AGTAATATTATTGCTCTGACACACACCCTTCTGCTCATTCAATTGCTCTTCTGTAACCACAA
 CACTCTCCCACTTCTTCTGTGACTTGGCCCTCTGCTCAAACCTGTCCTGTTTCTGATACAT
 20 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCCTTTACACTC
 AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCCTGAGAGTATCTTCCACACAGGGAA
 AGTGGAAAAGCCTTCTCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC
 CATTGTAGGCGTGTACTTTTTCCCCTCTCCACTCACCTGAGGACACTGATAAGATTGGT
 GCTGTCCTATTCACTGTGGTGACACCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA
 25 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCCTTTGA (SEQ
 ID NO: 2)

AOLFR2 sequences:

- 30 MMMVLRNLSMEPTFALLGFTDYPKQLQIPLFLVLLMYVITVVGNLGMIIHKINPKFHPTPMYFFL
 SHLSFVDFCYSSIVTPKLEENLVMADKSIFYFSCMMQYFLSCTAVVTESELLAVMAYDRFVAIC
 NPLLYTVAMSQRLLCALLVAGSYLWGMFGPLVLLCYALRLNFSGPVNVINHFFCEYALISVSGS
 DILPHLLLSFATFNEMCTLLIILTSYVFIVTVLKIRSVSGRHKAFSTWASHLTAITIFHGTLFL
 YCVPSNKSNSRQTVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:
 3)
- 35 ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCCACTTTGCCCTTTTAGGTTTTCACAG
 ATTACCCAAAGCTTCAGATTCCTCTCTTCTTGTGTTTCTGCTCATGTATGTTATCACAGTG
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAACCCCAAATTCACACTCCTATGT
 ACTTTTTCTTCTAGTCACCTCTCTTTTGTGTTTCTTGTACTCTTCCATTGTCACTCCCAAGC
 40 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA
 CTTCTGTCCTGCACTGCTGTGGTGACAGAGTCTTCTTGTGCTGGCAGTGATGGCCTATGAC
 CGCTTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTCACAGAGGCTCTGTG
 CCCTGCTGGTGGCTGGGTCATATCTCTGGGGCATGTTTGGCCCTTGGTACTCCTTTGTTAT
 GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACCTCTTTTGTGAGTATACTGC
 45 TCTCATCTCTGTGTCTGGCTCTGATATACTCATCCCCACCTGCTGCTTTTACAGCTTCGCCA
 CCTTCAATGAGATGTGTACACTACTGATCATCCTCACTTCCTATGTTTTCATTTTGTGACT
 GTACTAAAAATCCGTTCTGTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCTCCCAAC
 TGACTGCTATCACCATCTTCCATGGGACCATCCTTTTCTTTACTGTGTACCCAACTCCAAA
 AACTCTCGGCAAAACAGTCAAAGTGGCCTCTGTATTTTACACAGTTGTCAACCCCATGCTGA
 50 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACA
 TACACAAGTTCCATTTCACTGA (SEQ ID NO: 4)

AOLFR3 sequences:

- 55 MLLTDRNTSGTTFLLGFSDPQLQVPLFLVFLAIYNVTVLGNIGLIVIIKINPKLHTPMYFFLSQ
 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFFCTFVVTESELLAVMAYDRFVAICNPL
 LYTVDMSSQKLCVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHFFCEFSLLSLSCSDTYI

NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITFHGTILFLYCV
 PNSKNSRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)

5 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCCTCTTGGGCTTCTCAGATT
 ACCCAGAACTGCAAGTCCCACTCTTCCTGGTTTTTCTGGCCATCTACAATGTCAGTGTGCTA
 GGGAAATATTGGGTTGATTGTGATCATCAAATCAACCCCAAACTGCATACCCCATGTACT
 TTTTCCTCAGCCAACTCTCCTTTGTGGATTTCTGCTATTCTCCATCATTGCTCCCAAGATG
 TTGGTGAAACCTTGTGTCAAAGACAGAACCATTTTCATTTTTAGGATGCGTAGTACAATTCT
 TTTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTTATTAGCTGTGATGGCCTATGACCGC
 10 TTCGTGGCCATTTGCAACCCCTCTGCTCTACACAGTTGACATGTCCAGAACTCTGCGTGC
 TGCTGGTTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCTTGGAACTGACGTGCTCTGC
 TTTAAAGTTATGTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC
 TACTCTCCCTTTCTTGTCTGTACTTACATCAACCAAGTGGCTGCTATTCTTTCTTGCCACC
 TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT
 15 CCTCAAGATGCGTTCAGTCAGTGGGCGCCGCAAGCCTTCTCCACCTGTGCTCCCACTG
 ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTTTACTGTGTGCCCAACTCCAAAA
 CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCATGTTGAAT
 CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC
 ACCAAAGTCTTCTTACTGA (SEQ ID NO: 6)

20

AOLFR4 sequences:

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS
 LLDVMFSSVVPKVVDTLSKSTTISLKGCLTQLFVEHFFGGVGIILLVMAYDRYVAICKPLHY
 TIIMSPRVCCMLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIDHFCIDLFQLLLACTDTHILGL
 25 LVTNLNSGMMCVAFILILIASYTVILCSLSKSYSSKGRHKALSTCSSHLTVVVLFVPCIFLYMRPV
 VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

ATGGAAAATCAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC
 TGTGGAAAATATTTTCTGCTGTGTTTCTTGTGTCATGTATGTAGCCACAGTGTGGAAAATCT
 30 ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTACCTATGTATTTTTTTCTTA
 CCTTCTTGTCCCTTTTGGATGTCATGTTCTCATCTGTCGTGCCCCCAAGGTGATTGTAGAC
 ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTACCCAGCTGTTTGTGGAGC
 ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC
 CATCTGTAAGCCCTGCACTACAGATCATCATGAGTCCACGGGTGTGCTGCCTAATGGTA
 35 GGAGGGGCTTGGGTGGGGGATTTATGCACGCAATGATACTTCTCTTATGTATCAAAA
 TACCCTTCTGTGGTCTTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA
 CTTGCCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCTCAACAGTGGGATGATGT
 GTGTGGCCATCTTTCTTATCTTAATTGCGTCCTACACGGTCATCCTATGCTCCCTGAAGTCT
 TACAGCTCTAAAGGGCGGCACAAAGCCCTCTACCTGCAGCTCCCACCTCAGGTGGTTG
 40 TATTGTTCTTTGTCCCTGTATTTCTTGTACATGAGGCCTGTGGTCACTACCCCATAGAC
 AAGGCAATGGCTGTGTGACACTCAATCATCACACCCATGTTAAATCCCTTGATCTATACAC
 TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG
 CTGGGAAATAA (SEQ ID NO: 8)

45 **AOLFR5 sequences:**

MGKENCTTVAEFILLGLSDVPELRVCLFLLFLIYGVTLANLGMIALIQVSSRLHTPMYFFLSH
 LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLAVMAYDRFVAICNPL
 LYVTMTSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHFFCDLPVLSLACSDITVN
 ETLLFLVATLNEVSTIMILTSYLLLTILKMGSAEGRHKAFSTCASHLTAITVFHGTVLSIYCRP
 50 SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCATTCTCCTTGGACTATCAGATGTCC
 CTGAGTTGAGAGTCTGCCTCTTCTGCTGTTCTTCTCATCTATGGAGTCAGTTGTTAGCC
 AACCTGGGCATGATTGCACTGATTCAAGTCAAGTCTCGGCTCCACACCCCATGTACTTTT
 55 TCCTCAGCCACTTGTCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG
 GCTAATATCTTTAAACAAGGACAAAGCCATCTCCTTCTAGGGTGCATGGTGAATTCTACT

TGTTTTGCACCTTGTGTGGTCACTGAGGTCCTTCTGCTGGCCGTGATGGCCATGACCGCTTT
 GTGGCCATCTGTAACCCCTTTGCTATACACAGTCACCATGTCTTGAAGGTGCGTGTGGAGC
 TGGCTTCTTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCACTTTGTGCTTAGCTCTT
 AGGATCCCCCTTCTATAGATCTAATGTGATTAACCACTTTTTCTGTGATCTACCTCCTGTCTT
 5 AAGTCTTGCTTGCTCTGATATCACTGTGAATGAGACACTGCTGTTCTGGTGGCCACTTTG
 AATGAGAGTGTACCATCATGATCATCTCACCTCCTACCTGCTAATTCTCACCACCATCCT
 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCCACCTCACA
 GCTATCACTGTCTTCCATGGAACAGTCCTTTCCATTTATTGCAGGCCAGTTCAGGCAATA
 GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACCTC
 10 TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
 CAAAATTCACCTCCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

MMASERNQSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
 15 HSLTDFCFSTVVPKLEENLVVEYRTISFSGCIMQFCFACIFGVTEFMLAAMAYDRFVAVCK
 PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLDLDFCESTFINNFICDHSVIVSASYSDPYIS
 QRLCFHIAIFNEVSSLIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITIFHGTLFLYCVPNP
 KTSSLIVTVASVFYTVAPMLNPLIYSLRNKDINNMFELVVTCLIYH (SEQ ID NO: 11)

20 ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG
 AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTTGTTCGTCTACACAGTCACTGTA
 GTGGGGAACCTGGGCATGATAATAATCATCAGACTCAATTCAAACTCCATACAATCATGT
 ACTTTTCTTAGTCACTTGTCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA
 CTGTTGGAGAACTTGGTTGTGGAATACAGAACCATCTCTTTCTGTTGTCATCATGCAAT
 25 TTTGTTTTGCTTGCATTTTTGGAGTGACAGAACTTTCAATGTTAGCAGCGATGGCTTATGAC
 CGTTTTGTGGCAGTTTGTAACCCCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC
 TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTT
 CTTCTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTATCTGTGACCACTCTGT
 AATTGTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA
 30 TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTTCACTACC
 ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC
 TGACAGCCATCACTATCTCCATGGAACATCCTTTTCTTTACTGTGTCTTAATCCTAAA
 ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
 ACCCATGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT
 35 CACCAAATTGATTTACCACTGA (SEQ ID NO: 12)

AOLFR7 sequences:

MSYFYRLKLMKEAVLVKLPFTSLPLLQTLRKSRLDMEIKNYSSSTSGFILLGLSSNPQLQKPLF
 40 AIFLIMYLLAAVGNVLIIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLSETKVISY
 VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL
 FRVLLMSRLSFCASHIHKHFCDTQPVLKLSGSDTSSSQMVVMTETLAVIVTPFLCIFSYLRIMV
 TVLRIPSAAGKWKAFTSCGSHLTAVALFYGSIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN
 PFIYSLRNKDMKRGKLLQDRIYR (SEQ ID NO: 13)

45 ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTTA
 CATCTCTCCCACTGCTTCTCCAAACCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
 CTACAGCAGCAGCACCTCAGGCTTCATCTCCTGGGCTCTCTTCCAACCTCAGCTGCAG
 AAACCTCTCTTTGCCATCTTCCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT
 CATCCCGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACTTTTTTCTCAGCAACT
 50 TGTCTTTTATGGATATCTGCTTCAACAGTCATAGTGCTAAGATGCTGGTGAATTTTCTA
 TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTTATGGCAT
 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG
 CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT
 TCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGCTTGTCTTT
 55 CTGTGCCTCTCACATCATTAAAGCACTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
 GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCAATTGTGAC

CCCCCTCCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCCT
 CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCCACCTCACTGCAGTAGCCCT
 TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTACTCAGTGGTTAGGG
 ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCTTTCATCTACAG
 5 CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
 A (SEQ ID NO: 14)

AOLFR8 sequences:

MATSNHSSGAEFILAGLTQRPELQLPLFLFLGIYVVTVVGNLGMIFLIALSSQLYPPVYFLSH
 10 LSFIDLCYSSVITPKMLVNFVPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLLY
 NIVMSHRVCSIMMAVVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI
 LLFIUGGVNTLATTLAVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMYFKPPSS
 TTMEKEKVSSVFYITIIPMLNPLIYSLRNKDVKNALKKMTGRQSS (SEQ ID NO: 15)

ATGGCTACTTCAAACCATTCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC
 CAGAACTTCAACTGCCACTCTTCCTCCTGTTCCTTGAATATATGTGGTCACAGTGGTGGG
 GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCCTCCAGTGTATTATT
 TTCTCAGTCATTTGTCTTTTCATTGATCTCTGCTACTCCTCTGTCAATTACCCCTAAGATGCTG
 GTGAACCTTGTTCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT
 20 CTTCTTATTTTTGTAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT
 GTTGTATCTGTGCGCCACTGCTTTACAATATTGTCAATGTCCACAGGGTCTGTTCCATAAT
 GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA
 GTGTTGTCACTCTGTAGGTCTCATACGGTCAGTCATTATTTTGTGATATTCTCCCTTATT
 GACTCTGTCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTTCATTATTGGAGGAGTT
 25 AATACCTTAGCAACTACACTGGCGGTCTTATCTCTTATGCTTTTCATTTTCTTAGTATCCT
 TGGTATTCACTCACTGAGGGGCAATCCAAAGCCTTTGGCACTGTAGCTCCCATCTCTTG
 GCTGTGGGCATCTTTTTTGGGTCTATAACATTCTATGATTTTCAAGCCCCCTTCAGCACTAC
 TATGGAAAAAGAGAAGGTGTCTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT
 CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
 30 AGGCAGTCATCCTGA (SEQ ID NO: 16)

AOLFR9 sequences:

MLARNNSLVTEFILAGLTDRPEFWQPFFFLFLVIYIVTMVGNLGLITLFGNLNSHLHTPMYYFLFN
 LSFIDLCYSSVFTPKMLMNFVSKKNISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
 35 LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHLYCDILPLLQLSCTSTYV
 NEVVVLIVVGTNITVPSCITILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY
 SSGSMEQKGVFSVFYTNVPMPLNPLIYSLRNKDVKVALRKALIKIQRNIF (SEQ ID NO: 17)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAAACAGATCGTC
 CAGAGTTCTGGCAACCCTTCTTTTTCTGTTTCTAGTGATCTACATTGTCACCATGGTAGGC
 AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTAATTT
 CCTCTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT
 GAACCTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC
 TTTCTCTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT
 45 GGCCATCTGTAATCCATTGCTGTATAAGGTCAACCATGTCCCATCAGGTCTGTTCTATGCTCA
 CTTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGTTTAG
 ACTCACCTTCTGCAGTGCTAATATCATTAACCATTACTTGTGTGACATACTCCCCCTCCTCC
 AGCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTACTAA
 TATCACGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTCATTGTCAGTACTAGCATTCTC
 50 ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCATTGC
 TCTGTCTCTGTTTTTTGGGTCAGCGGCATTGATGATATTAATATTCTTCTGGATCTATGG
 AGCAGGGAAAAAGTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCCTCATC
 TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAATTCAG
 AGGAGAAATATATTCTAA (SEQ ID NO: 18)

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AOLFR10 sequences:

MLARNNSLVTEFILAGLTDRPEFRQPLFFLFLVYIVTMVGNLGLILFGLNSHLHTPMYYFLFNL
 SFIDLCYSSVFTPKMLMNFVSKNIIISYVGCMTQLFFFLFFVISECYILTSMA YDRYVAICNPPLY
 KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMLRLTFCSANIINHYLCDILPLLQLSCTSTYVN
 5 EVVVLIVVGINIMVPSCTILISYVFIVTSLHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS
 SGSMEQKGVSSVFYTNVPMNLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
 CAGAGTTCGGCAACCCCTCTTTTCTGTTTCTAGTGATCTACATTGTCACCATGGTAGGC
 10 AACCTTGGCTTGATCATTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
 CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCTCTGTTTTCACTCCAAAATGCTAAT
 GAACTTTGTATCAAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTCT
 TTCTCTTTTTTGTCATCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
 GCCATCTGTAATCCATTGCTGTATAAGGTACCATGTCCCATCAGGTCTGTTCTATGCTCAC
 15 TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGCTTAGA
 CTCACCTTCTGCAGTGCTAATATCATCAACATTACTTGTGTGACATACTCCCCCTCTCCA
 GCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTATTAAT
 ATCATGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTATTGTCACCTAGCATTCTTCA
 TATCAAATCCACTCAAGGAAGATCAAAAAGCCTTCAGTACTTGTAGCTCTCATGTCATTGCT
 20 CTGCTCTGTTTTTTGGGTCAGCGGCATTGATGATATTAATAATTCTTCTGGATCTATGGA
 GCAGGGAAGAAAGTTTCTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCTCTCATCT
 ACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAGA
 GAAGAAATATATTCTAA (SEQ ID NO: 20)

AOLFR11 sequences:

MTLRNSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLFNLS
 FIDLCYSCVFTPKMLNDFVSEIISYVGCMTQLFFFCFFVNSECYVLVSMAYDRYVAICNPPLY
 MVTMSPRVCFLLMFGSYVVGAGAMAHTGSMLRLTFCDNSVIDHYLCDVLPPLLQLSCTSTHV
 30 SELVFFIVVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSIIAVALFFGSGTFTYLTTS
 FPGSMNHGRFASVFYTNVPMNLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTGGGATTATCAGAACAGC
 CAGAGCTCCAGCTCCCTCTTTTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC
 AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCCATGTACTTTTT
 35 CCTCTCAACTTGTCTTTATAGATCTCTGTTATTCTGTTGTTTACCCCCAAAATGCTGA
 ATGACTTTGTTTCAGAAAGTATCATCTCTTATGTGGGATGTATGACTCAGCTATTTTTCTTC
 TGTCTCTTTGTCAATTCTGAGTGCTATGTGTTGGTATCAATGGCCTATGATCGCTATGTGGC
 CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCAAGGGTCTGCTTTCTGCTGATGT
 TTGGTTCCTATGTGGTAGGGTTTGCTGGGGCCATGGCCACACTGGAAGCATGCTGCGACT
 40 GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTGCAAGC
 TCTCCTGCACCAGCACCCATGTCAGTGAGCTGGTATTTTTTATTGTTGTTGGAGTAATCACC
 ATGCTATCCAGCATAAGCATCGTCATCTTACGCTTTGATACTCTCCAACATCCTCTGTAT
 TCCTTCTGCAGAGGGCAGATCCAAAGCCTTTAGCATATGGGGCTCCACATAATTGCTGTT
 GCTCTGTTTTTTGGGTCAGGGACATTCACCTACTTAACAACATCTTTTCTGGCTCTATGAA
 45 CCATGGCAGATTTGCCTCAGTCTTTTACACCAATGTGGTTCCCATGCTTAACCCCTCGATCT
 ACAGTTTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAACCCTGAAGAGAGTGCTCT
 TCTAA (SEQ ID NO: 22)

AOLFR12 sequences:

MERNHNPDCNVLNFFADKKNKRRNFGQIVSDVGRICYSVLSLGEPTTMGRNNLTRPSEFIL
 LGLSSRPEDQKPLFAVFLPIYLITVIGNLLILAIRSDTRLQTPMYFFLSILSFVDICYVTVIIPKMLV
 NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMAIDRYVAICNPFHYITIMSHRCCVLLLVLS
 FCIPIHFHSLHILLTNQLIFCASNVIIHFFCDDQPVLLKSCSSHVFKEITVMTEGLAVIMTFPSCIII
 55 SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP
 MLNPFYISLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

ATGGAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTTCTTTGCTGATAAGA
 AGAATAAAAGGAGAAATTTTGGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG
 TTAGTTTATCTTTAGGTGAACCCACAACCTATGGGAAGAAATAACCTAACAGACCCTCTGA
 ATTCATCCTCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC
 5 TCCCCATCTACCTTATCACAGTGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA
 CACTCGTCTCCAGACGCCCATGTACTTCTTTCTAAGCATCCTGTCTTTGTGACATTTGCT
 ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTTCTTATCAGAGACAAAGACCATCTC
 TTACGGTGAGTGTCTGACCCAGATGTACTTTTTCTTAGCCTTTGGAAACACAGACAGTTAC
 CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA
 10 CCATTATGAGTCACAGATGCTGTGCTGCTTCTGGTTCTCTCCTTCTGCATTCCACATTTT
 CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA
 TCATTTTTCTGCGATGATCAACCAGTGCTAAAATTGCTCTGCTCCTCCCATTTTGTCAAAG
 AAATCACAGTAATGACAGAAGGCTTGCTGTGCTAATGACCCCGTTTTTCATGCATCATCAT
 CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCCTTCAGCTGCTGGAAAGCGTAAA
 15 GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCTGTTTTATGGAAGCATTAGCTA
 TGTCTATTTTACGCCCTGTCCAACATACTGTCAAGGATCAAATAGCAACAATTATCTAC
 ACCGTACTGACTCCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC
 AGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

20 **AOLFR13 sequences:**

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYIFTLLGNKTIIVLSHLDPHLHNP MYFFFSNL
 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL
 HYTVVMHPCLYVLMASWSWVIGFANSLLQTVLILLTLGCRNKLEHFLCEVPPLLKLACVDTT
 MNESELFVSVIILLVPVALIIFSYSQIVRAVVRIKSATGQRKVFGTCGSHLT VVSFLFYGTAIYAY
 25 LQPGNNYSQDQGXISLFYTIITPMPINPLYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:
 25)

ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTATCCTACTGGGTTTCTCTGACAGGC
 CTCAGCTGGAGCTAGTCCTCTTTGTGGTTTCTTTGATCTTCTATATCTTCACTTTGCTGGGG
 30 AACAAAACCATCATTGTATTATCTCACTGGACCCACATCTTCACAATCCTATGTATTTTTT
 CTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG
 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTGTGTAGTTCACTGTACAT
 CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT
 GCAGCTGTTTGCAGGCCCTCCACTACACAGTAGTCATGCACCCCTGTCTGTATGTGCTGA
 35 TGGCTTCTACTTCATGGGTCAATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG
 CTTTAAACACTTTGTGGAAGAAATAAATTAGAACACTTCTTTGTGAGGTTCCTCCATTGCT
 CAAGCTTGCTGTGTTGACACTACTATGAATGAATCTGAACCTCTTCTTGTGAGTGCTCATTA
 TTCTTCTGTACCTGTGTGATTAATCATATTCTCCTATAGTCAGATTGTCAGGGCAGTCGTG
 AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTGTTGGGACATGTGGCTCCACCTCACA
 40 GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTACCTCCAGCCCGGCAACAACCTACTC
 TCAGGATCAGGGCAAGKTCATCTCTCTTCTACACCATCATTACACCCATGATCAACCCC
 CTCATATATACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
 AACTACGACTCCAGATGA (SEQ ID NO: 26)

45 **AOLFR14 sequences:**

MALPLLLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL
 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSSAIGPKMLVDLLPRATIPYTACALQMF
 VFLAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRLCLALLGASGLGGA VSAFVHTTLTF
 RLSFCRSRKINSFFCDIPLLAISCSDSLNE LLFAICGFIQTATVLAITVSYGFIA GAVIHMRSVE
 50 GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALD TDKMASVFYTLVIPSLNPLIYSLRNKE
 VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG
 GATGAACTCAGAGAACCTCACCCGGGCGCGGTTGCCCTGCTGAATTCGTCTCTCTGGGC
 55 ATCACAAATCGCTGGGACCTGCGTGTGGCCCTCTCCTGACCTGCCTGCTGTCTACCTGG
 TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCCGGCTCCACA

CACCTATGTACTTCTTCTGCGCAACCTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATC
 GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCCGAGCCACCATCCCTTACACAGCCTGTG
 CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTGCTTGGTGGCAGCCAT
 GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATAACAACAGCTATGTCGCAG
 5 CGTCTATGCCTGGCCTTGTGTTGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTTT
 ACACAACCCCTCACCTTCCGCTGAGCTTCTGCGCTCCCGGAAGATCAATAGCTTCTTCTG
 CGATATCCCTCCACTGCTGGCCATCTCGTGACGTGACACCAGTCTCAATGAACTCCTTCTCT
 TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTTAGCTATCACGGTGTCTTATGGCTT
 CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGCGAGGGCAGTCGGCGAGCAGCCTCCAC
 10 CGGTGGTTCCCACTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG
 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG
 TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
 CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCAGTGA (SEQ ID NO: 28)

15 **AOLFR15 sequences:**

MRENNQSSSTLEFILLGVTGQQEQEDFFYLFLFIYPITLIGNLLIVLAICSDVRLHNPMPYFLLANLS
 LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYLAAMAYDRAVAISHPLH
 YTTIMSPRSCIWLIAGSWVIGNANALPHILLTASLSFCGNQEVANFYCDITPLKLSCDIHFHV
 KMMYLGVGIFSVPLLCIIVSYIRVFSTVFQVPSTKGVLFKAFSTCGSHLTVVSLYYGTVMGTYFR
 20 PLTNYSLKDAVITVMTAVTPMLNPFYISLRNRMKAALRKLFNKRIS (SEQ ID NO: 29)

ATGAGGGAAAATAAACCAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC
 AGGAACAGGAAGATTTCTTCTACATCCTCTTCTGTTCAATTTACCCCATCACATTGATTGGA
 AACCTGCTCATTGTCCTAGCCATTTGCTCTGATGTTTCGCCTTCACAACCCCATGTATTTTCT
 25 CCTTGCCAACTCTCCTTGGTTGACATCTTCTTCTCATCGGTAACCATCCCTAAGATGCTGG
 CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT
 CATGATAGCCTTGGGTAACACAGACAGCTATATTTTGGCTGCAATGGCATATGATCGAGCT
 GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTGTATCTGGC
 TTATTGCTGGGTCTTGGGTGATTGGAATGCCAATGCCCTCCCCACACTCTGCTCACAGC
 30 TAGTCTGTCCTTCTGTGGCAACCAGGAAGTGGCAACTTCTACTGTGACATTACCCCTTG
 CTGAAGTTATCCTGTTCTGACATCCACTTTCATGTGAAGATGATGTACCTAGGGGTGGCA
 TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTCGAGTCTTCTCCACAGTCTTCC
 AGGTTCCCTCCACCAAGGGCGTGCTCAAGGCCCTTCTCCACCTGTGGTTCCCACTCACGGT
 TGCTCTTTGTATTATGGTACAGTCATGGGCACGATTTCCGCCCTTTGACCAATTATAGCC
 35 TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTAAATCCTTTCAT
 CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT
 CTCTCGTAA (SEQ ID NO: 30)

AOLFR16 sequences:

40 MRRNCTLVTEFILLGLTSRRELQILLFTFLAIYMTVAVAGNLGMIVLIQANAWLHMPMYFFLSH
 LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLVCYLFIALVHVEIYILAVMAFDYMAICNP
 YGSRMSKSVCSFLITVPYVYGALTGLMETMWTYNLAFCGPNEINHFCADPPLIKLACSDTYN
 KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR
 PPSKESVEQGMVAVFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

45 ATGAGAAGAACTGCACGTTGGTGACTGAGTTCACTCTCCTGGGACTGACCAGTCGCCGG
 GAATTACAAATTCTCCTCTTACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA
 ACCTTGGCATGATTGTCCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTC
 CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTTCCAATGTGACTCCAAAGATGCTGG
 50 AGATTTTCTTTTCAGAGAAGAAAAGCATTTCTATCCTGCCTGTCTGTGCAAGTGTACCTT
 TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT
 GGCCATCTGCAACCCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCCTC
 ATCACGGTGCCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA
 ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT
 55 TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG
 AACCTTTCTTTTCTCTCTTCATCATATGTATTTCTACCTTTACATTTTCCCTGCTATTTTA

AAGATTTCGCTCTACAGAGGGGCAGGCAAAAAGCTTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCCTTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT
GTTGAACAGGGTAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTA
TAATTTATAGCCTTAGAAATAAAAATGTAAAAGAAGCATTAATCAAAGAGCTGTCAATGA
5 AGATATACTTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

MLNFTDVTEFILLGLTSRREWQVLFIFLHVYIITMVGNI GMMVLIKVSPQLNNPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDDKKTITYAGCLVQCFIFIALVHVEIFILAAMAFDRYMAIGNPLL
10 YGSKMSRVVCIRLITFPYIYGFLTSLAATLWTYGLYFCGKIEINH FYCADPPLIKMACAGTFVKE
YTMILAGINFTYSLTVIISYLFILAILRMRS AEGRQKAFSTCGSHLTA VIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT
15 GGCAAGTTCCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCAACCATGGTGGGCAATATC
GGCATGATGGTGTAAATCAAGGTCAGTCCTCAGCTTAACAACCCCATGTACTTTTCTCTCA
GTAATTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAC
CTGTTTTTCAGATAAAAAACAATTACTTATGCTGGTTGTTTAGTACAGTGTTCCTTCTTCAT
TGCTCTTGTCATGTGGAATTTTATTCTTGCTGCGATGGCCTTTGATAGATACATGGCAA
20 TTGGGAATCCTCTGCTTTATGGCAGTAAAATGTCAAGGGTTGTCTGTATTGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGGAATAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACCTC
ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
25 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 34)

30

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLFLVFLVYVLTLLGNLGMIMLMRLDSRLHTPMYFFLT
NLAFVDLCYTSNATPQMSNIVSEKTISFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFSDGLFQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK
35 EHAMFISAGFNLSSSLTIVLVSYAFILAAILRIKSAEGRHKAFTSCGSHMMAVTLFYGTLCMYI
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC
CGGAACTCCAGTCTCTGCTTTTTGTGCTGTTTCTGGTTGTTTACCTCGTACCCTGCTAGGC
40 AACCTGGGCATGATAATGTAAATGAGACTGGACTCTCGCCTTCACACGCCCATGTAATTCT
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTTCTTTGCTGGTTGCTTTACACAGTGCTACATTT
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG
45 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCTGACCTTCCG
CCTGACCTTCTGTAGATCCAATGTCAATCAACCACTTCTACTGTGCTGACCCGCCGCTCATT
AGCTTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTCATATCTGCTGGCTTCAAC
CTCTCCAGCTCCCTCACCATCGTCTTGGTGTCTTATGCCTTCATTCTTGTGCTGCCATCCTCCG
GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCTATATGATGGC
50 TGTACCCCTGTTTATGGGACTCTCTTTGTCATGTATATAAGACCACCAACAGATAAGACT
GTTGAGGAATCTAAATAATAGCTGTCTTTACACCTTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCCTGAGATGA
(SEQ ID NO: 36)

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AOLFR19 sequences:

METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLILAIYSDPRLHTPMYFFLSNL
 SFMDICFTTVIVPKMLVNFLSETKIISYVVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
 YDVVMKPWHCLLMMLGSCSISHLHSLFRVLLMSRLSFCASHIHKHFFCDTQPVVLKLSCDTSSSQ
 5 MVMVTETLA VIVTPFLCTIFS YLQIIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFGSVTVYVYFR
 PLSMYSVMKGRVATVMYTVVTPMLNPFYISLRNKDMKRGLKKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCTCTCTTCCA
 ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCTCATCATGTACCTACTCACTGCGGTG
 10 GGAATGTGCTCATCATCCTGGCCATCTACTCTGACCCCAGGCTCCACACCCTATGTACT
 TTTTCTCAGCAACTTGTCTTTCATGGATATCTGCTTCACAACAGTCATAGTGCCTAAGATG
 CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT
 ACTTCTCATGGCATTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
 15 CTCATGCTATTGGGTCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTAT
 GTCTCGCTTGTCTTCTGTGCCTCTCACATCATTAAAGCACTTTTCTGTGACACCCAGCCTG
 TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
 AGCTGTCAATTGTGACCCCTTCTGTGTACCATCTTCTCCTACCTGCAAATCATCGTCACTG
 TGCTCAGAATCCCCTCTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCACCT
 20 CACTGTAGTGGTCTTCTATGGGAGTGTCTATGTCTATTTTAGGCCTCTGTCCATGT
 ACTCAGTGATGAAGGGCCGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA
 ACCCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGAC
 ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

MVEENHTMKNEFILTGFTDHPKLTLLFVVFVFAIYLITVVGNISLVALIFTHCRLHTPMYIFLGN
 LALVDSCCACAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP
 LQYHMMSSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHINHFYCDTLPYRLSCVDPF
 30 INELVLFIFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFLYIRP
 NLEEGGNDIPAAILFTIVVPLNPFYISLRNKEVISVLRKILLKIKSQSGSVNK (SEQ ID NO: 39)

ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC
 CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCCTGGTGGG
 GAATATTAGTTTGGTGGCACTGATATTACACACTGTCGGCTTCACACACCAATGTACATC
 35 TTCTGGGAAATCTGGCTCTTGTGGATTCTTGTCTGTGCTGTGCTATTACCCCCAAAATGTT
 AGAGAACTTCTTTTCTGAGGGCAAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTTAT
 TTCTTTGCACTGTGGAACTGCAGACTGCTTTCTTCTGGCAGCAGTGGCCTATGACCGCT
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAACTCTGCATTCA
 GATGACCACAGGCGCCTTCATAGCTGGAAATCTGCATTCCATGATTGATGATAGGGCTTGTA
 40 TTAGGTTAGTTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT
 GTATAGACTCTCCTGTGTTGACCCCTTTCATCAATGAACTGGTCTATTCTCTCAGGTT
 CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTTACTATT
 TTCAGAAATGAAATCCAAGGAGGGAAGGCCAAAGCCTTTTCTACTTGTGCATCCCACTTTT
 CATCAGTTTCATTATTCTATGGATCTATTTTTTCTCTATACATTAGACCAAATTTGCTTGAA
 45 GAAGGAGGTAATGATATACCAGCTGCTATTTTATTTACAATAGTAGTTCCTTACTAAATC
 CTTTCATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATCTGCTGAA
 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

MEPRKNVTDVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTVSETLGSPMSFFLAGL
 50 TFIDIYSSSISPRLLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLLVMAYDRYVAICKPLHYLV
 IMRQWVCVLLLVVSWVGGFLQSVFQLSIYGLPFCGPNVIDHFFCDMYPLLLACTDTHVIGLL
 VVANGGLSCTIAFLLLISYGVILHSLKKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR
 TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

55

TCACCCTCTCCTTCTGTAAAGGACAAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG
 CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT
 TTGTGATTTTGGCCAATGCCTCCGTATCCTGATTTCCTATCTGCTCATCATCAAGACCATT
 TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA
 5 CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA
 TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC
 CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGA
 GACTCCAGGTGTCCTGAGCATGTAG (SEQ ID NO: 46)

10 **AOLFR25 sequences:**

METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITVMGNLIITVTSDSLHTPMYFLLRN
 LAVLDLCFSSVTAPKMLVDLLSEKKTISYQCGMGQIFFHFLGGAMVFFLSVMAFDRLIAISRPL
 RYVTVMNTQLWVGLVWVATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVLRLACTDT
 SLLEFLKISNSGLLDVVWFLLMSYLFILVMLRSHPGEARRAASTCTTHIIVSMIFVPSIYLY
 15 ARPFTFPMDKLVSIGHTVMTPLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCTGCGGCTCTCGCAGACTC
 GGGAGCTCCAGCGTTTCTGTTTCTAATGTTCTGTTTGTCTACATCACCAGTGTATGGGA
 AACATCCTTATCATCATCACAGTGACCTCTGATTCCAGCTCCACACACCCATGTACTTTCT
 20 GCTCCGAAACCTGGCTGTCTAGACCTCTGTTTCTTCTCAGTCACTGCTCCCAAAATGCTAG
 TGGACCTCCTCTCTGAGAAGAAAACCATCTCTACCAGGGCTGCATGGGTGAGATCTTCTT
 CTTCCACTTTTTGGGAGGTGCCATGGTCTTCTTCTCTCAGTGATGGCCTTTGACCGCCTCA
 TTGCCATCTCCCGGCCCTCCGCTATGTCACCGTCATGAACACTCAGCTCTGGGTGGGGCT
 GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC
 25 CCACTGCCCTTCTGTGGCCCCAACATTTTGATAACTTCTACTGTGATGTTCCCCAAGTACT
 GAGACTTGCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG
 CTGGATGTCGTCTGGTCTTCTCTCTCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG
 GTCACATCCAGGGGAGGCAAGAAGGAAGGACGCTTCCACCTGCACCAACCATCATCGT
 GGTTTCCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA
 30 TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCATGCTCAACCCCATGATCTA
 TACCCTGAGGAACAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
 TTGA (SEQ ID NO: 48)

AOLFR26 sequences:

35 MAAKNSSVTEFILEGLTHQPLRIPFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS
 LIDFCFSTTTTPKMLMSFVSRKNISFTGCMTQLFFFCFFVSESFILSAMAYDRYVAICNPLLYT
 VTMSQVCLLLLLGAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILPLELSCNSSYMN
 ELVVFIVVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIIVSLFFGSGAFMYLKP
 LSILPLEQGVSSLFYTIIVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

40 ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG
 GACTGCGGATCCCCCTCTTCTTCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA
 CCTGGGCTTGATAACCTGATTGGGCTGAACCTCACCTGCACACTCCCATGTACTTCTTCC
 TTTTAACTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG
 45 AGTTTTGTCTCAAGGAAGAACATCATTCCTTCACAGGGTGTATGACTCAGCTCTTCTTCTT
 CTGCTTCTTTGTCTCTCTGAGTCCTTCATCTGTGTCAGCGATGGCGTATGACCGCTACGTGG
 CCATCTGTAAACCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGCTCCTTTTG
 TTGGGTGCCTATGGGATGGGGTTTGTCTGGGGCCATGGCCACACAGGAAGCATAATGAAC
 CTGACCTTCTGTGCTGACAACCTTGTCAATCATTTTCATGTGTGACATCCTTCTCTCTTGA
 50 GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC
 GTTGGAATGCCCATTGTCACTGTCTTTATTTCTTATGCCCTCATCTCTCCAGCATTCTACA
 CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAAGTCCACATAATTGTA
 GTTTCTCTTTTCTTTGGTTCTGGTGCTTTTCATGTATCTCAAACCCCTTTCCATCCTGCCCTC
 GAGCAAGGGAAAAGTGTCTCCTGTTCTATACCATAATAGTCCCGGTGTTAAACCCATTAA
 55 TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA
 TCTTTTCTTAA (SEQ ID NO: 50)

AOLFR27 sequences:

MPSQNYSHSEFNLFGFSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATTWIEHRLHTPMYFLCTL
 SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR
 5 YNVLMSPRDCAHLVACTWAGGSVMGMMVTITVFHLTFCGSNVIIHFFCHVLSLLKLACENKT
 SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKTFSTCVSHLTVVVTHYSFASFIY
 LKPKGLHSMYSDALMATTYTVFTFPLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:
 51)
 10 ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC
 CCAGCACCTCCTGCCCATCTTGTTCCCTGCTGTACCTCCTGATGTTCCCTGTTACATTGCTGG
 GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
 CTCTTGTCACCCCTCTCCGCTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC
 TGGCTGATCTGCTTTCCACCCATCATTCCATCACCTTTGTGGCTTGTGCCAACCAGATGTTT
 15 TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCTCTCTGGTCATGGGCTATGATCGCTA
 TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCCGTGAAGTGTGCCCAT
 CTGTGGCCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT
 TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTTTTCTGTGCTATGTGCTTTCCCTCT
 TGAAGTTGGCCTGTGAAAAAAGACATCATCTGTGATCATGGGTGTGATGCTGGTGTGTGT
 20 CACAGCCCTGATAGGCTGTTTATCTCTCATCATCTCTCTCTATGTCTTCATTGTGGCTGCCA
 TCTTGAGGATTCCCTCTGCCGAAGGCCGCAACAAGACATTTTCTACGTGTGATATCCACCT
 CACTGTGGTGGTCACGCACTATAGTTTTGCCTCCTTTATCTACCTCAAGCCCAAGGGCTCC
 ATTCTATGTACAGTGACGCCTTGATGGCCACCACCTATACTGTCTTCAACCCCTTCTTAGC
 CCAATCATTTTACGCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAAACTTTTACA
 25 GAAATTCTGTCTCTCAAGTTCCTGA (SEQ ID NO: 52)

AOLFR28 sequences:

MPNFTDVTEFTLLGLTCRQELQVLFFVFLAVYMITLLGNIGMIILISISPQLQSPMYFFLSHLSF
 ADVCFSSNVTPKMLENLLSETKTISYVGCLVQCYFFIAVVHVEVYILAVMAFDRYMAGCXPLL
 30 YGSKMSRTVCVRLISVXYXYGFSVSLICTLWYGLYFCGNFEINHFYCADPPLIQIACGRVHIKE
 ITMIVIAGINFTYSLSVLISYTLIVVAVLRMRSDGRRKAFSTCGSHLTAVSMFYGTPIFMYLR
 RPTESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)
 35 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTCTGTCAGGAGC
 TACAGGTTCTCTTTTTTGTGGTGTTCCTAGCGGTTACATGATCACTCTGTTGGGAAATATT
 GGTATGATCATTTTTGATTAGCATCAGTCCTCAGCTTACAGAGTCCCATGTACTTTTTCTGAG
 TCATCTGTCTTTTGCAGGAGTGTGCTTCTCTCCTCAACGTTACCCCCAAAATGCTGGAAAAT
 TATTATCAGAGACAAAACCATTTCTATGTGGGATGCTTGGTGACAGTGCTACTTTTTTCT
 TGCCGTTGTGCCAGTGGAGGTCTATATCTCTGGCTGTGATGGCCTTTGACAGGTAGGGCCTC
 40 GGCTGCAANCCTCTGCTTTATGGCAGTAAATGTCTAGGACTGTGTGTGTTCCGGCTCATCT
 CTGTGNNTATGNNTATGGATTCTCTGTGAGCCTAATATGCACACTATGGACTTATGGCTT
 ATACTTCTGTGGAACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA
 TTGCCTGTGGGAGAGTGACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACCTT
 CACATATTCCTCTCGGTGGTCCTCATCTCCTACACTCTCATTTGATAGCTGTGCTACGCA
 45 TGCGCTCTGCCGATGGCAGGAGGAAGGCGTTCTCCACCTGTGGGTCCCCTTGACGGCTGT
 TTCTATGTTTTATGGGACCCCATCTTATGTATCTCAGGAGACCCACTGAGGAATCCGTA
 GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCCTATGTTGAATCCCATGA
 TCTACAGTCTGAGAAATAAGGATGTAAAGAAGCAGTCAACAAAGCAATCACCAAGACAT
 ATGTGAGGCAGTAA (SEQ ID NO: 54)
 50

AOLFR29 sequences:

MMSFAPNASHSPVFLLLGFSRANISYTLFLFLAIYLTTLGNVTLVLLISWDSRLHSPMYLLR
 GLSVIDMGLSTVTLPLQLLAHLVSHYPTIPAARCLAQFFFFYAFGVTDTLVIAVMALDRYVAICD
 PLHYALVMNHQRCACLLALSWSVLSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLLR
 55 ASCSDIHSNELAIFFEAGFLMLGPCALIVLSYVRIGAAAILRLPSAAGRRRAVSTCGSHLTMVGFL

TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTA CTCTCATCAGTCACACCTGTCATGCTC
 ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCAGCTCTGTT
 CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCCTGCTGGCTGCCATGGCCTATGATCGCTA
 TGTGGCCATCTGCTCACCCTGCTCTACTCTACCTGCATGTCCCCTGGAGTCTGCATCATCT
 5 TAGTGGGCATGTCCTACCTGGGTGGATGTGTGAATGCTTGGACATTCAATTGGCTGCTTATT
 AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTTCTGTGACTATTCACCACTTT
 TGAAGCTTGCTTGTCCCATGATTTTACTTTTGAATAAATCCAGCTATCTCTTCTGGATCT
 ATCATTGTGGCCACTGTGTGTGCATAGCCATATCCTACATCTATATCCTCATCACCATCCT
 GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT
 10 GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCCAAGTCCAGCTACTC
 AACTGACCAGAACAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC
 CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
 AAAATATTTTCTTGA (SEQ ID NO: 60)

15 **AOLFR32 sequences:**

MNSLKDGNHTALTGFILLGLTDDPILRVILFMIILSGNLSIILIRISSQLHHPMYFFLSHLAFADM
 AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAFFATVECVLLAAMAYDRFVAICSPLLYSTK
 MSTQVSVQLLL VVYIAGFLIAVS YTSFYLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVVL SF
 SSGSIHVTV CVIAVCYIYILITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTTTFIYVMPNFSYST
 20 DQNKVSVSLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNDIT (SEQ ID
 NO: 61)

ATGAATTCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA
 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA
 25 ATTATTCTTATCAGAAATTTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT
 GGCTTTTGCTGACATGGCCTATTTCATCTTCTGTACACCCCAACATGCTTGTAAACTTCTTGG
 TGGAGAGAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTGAGCGGCTTTCTT
 TGCAACAGTCGAATGCGTCTTCTGGCTGCCATGGCCTATGACCGCTTGTGGCAATTTGC
 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG
 30 TTTACATAGCTGGTTTTCTCATTGCTGTCTCCTATACTACTTCTTCTATTTTTTACTCTTCT
 GTGGACCAAAATCAAGTCAATCATTTTTCTGTGATTTGCTCCCTTACTTGAAGTCTCCTGT
 TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTCTTCTGGATCCATCATGTGTCAC
 TGTGTGTGTGCATAGCCGTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA
 CTGAGGGGCACCACAAGGCCTTCTCCACCTGCACTTCCCACCTCACTGTGGTTACCTGT
 35 CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCACTGACCAGAAC
 AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC
 TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTAGAAAAATACTTTCTC
 ATGATGCTTGTATTTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

40 **AOLFR34 sequences:**

MLEGVEHLLLLLLTDVNSKELQSGNQTSVSHFILVGLHPPQLGAPLFLAFLVITYLLTVSGNG
 LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHLGCT
 ECFLYTLMA YDRFLAICKPLHYATIMTHRVCNSLALGTWLGGTIHSLFQTSFVFRLPFCGPNRV
 DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILTSYGYVAAILRIPSADGRRNAFST
 45 CAAHLTVVIVYVPCTFIYLRPCSQEPLDGVVAVFYTVITPLNLSIYTLCKEMKAALQRLGG
 HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG
 AACTGCAAAGTGAAACCAGACTTCTGTGTCTCACTTCATTTGGTGGGCCTGCACCACCC
 50 ACCACAGCTGGGAGCGCCACTCTTCTTAGCTTTCCTTGTGCATCTATCTCCTCACTGTTTCTG
 GAAATGGGCTCATCATCCTCACTGTCTTAGTGACATCCGGCTCCATCGTCCCATGTGCTT
 GTTCTGTGTACCTCTCCTTCTTGACATGACCAATTTCTGTGCTATTGTCCCCAAGATGC
 TGGCTGGCTTTCTCTGGGTAGTAGGATTATCTCCTTTGGGGGCTGTGTAATCCAACATTT
 TCTTTCCATTTCTGGGCTGTACTGAGTGCTTCTTCTTACACACTCATGGCTTATGACCGTTT
 55 CCTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC
 TGGCTTTAGGCACCTGGCTGGGAGGGACTATCCATTCACTTTTCCAAACAAGTTTTGTATT

CCGGCTGCCCTTCTGTGGCCCCAATCGGGTCGACTACATCTTCTGTGACATTCTGCCATGC
 TCGTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACCTTTGCAGACATTGGCTT
 CCTGGCCCTCACCTGCTTCATGCTCATCCTCACTTCTATGGCTATATTGTAGCTGCCATCC
 TGCGAATTCGCTCAGCAGATGGGCGCCGAATGCCTTCTCCACTGTGTGCTGCCACCTCAC
 5 TGTGTGTCATTGTTACTATGTGCCCTGCACCTTCATTACCTGCGGCCTTGTTCACAGGAGC
 CCCTGGATGGGGTGGTAGCTGTCTTTTACACTGTCATCACTCCCTTGCTTAACTCCATCATC
 TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA
 GTGCAGCCTCACTGA (SEQ ID NO: 64)

10 **AOLFR35 sequences:**

MEPLNRTEVSEFFLKGFSGYPALHLLFPLCSAMYLVTLLGNTAIMAVSVLDIHLHTPVYFFLG
 NLSTLDICYTPTFVPLMLVHLLSSRKTISFAVCAIQMCLSLSTGSTECLLAITAYDRYLAICQPL
 RYHVLMSHRLCVLLMGAAWVLCCLKSVTEMVISMRLPFCGHHVVSHTCKILAVLKLACGNT
 SVSEDFLLAGSILLPVPLAFICLSYLLILATILRVPSAARCKAFSTCLAHLAVLLFYGTIIFMY
 15 LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO:
 65)

ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTCTTTCTGAAAGGATTTTCTGGCTACC
 CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCCCTCTGGG
 20 GAACACAGCCATCATGGCGGTGAGCGTGTAGATATCCACCTGCACAGCCCGTGTACTTC
 TTCCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCACCTTTGTGCTCTGATGCT
 GGTCCACCTCCTGTATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC
 TGAGCCTGTCCACGGGCTCCACGGAGTGCCTGCTACTGGCCATCACGGCCTATGACCGCTA
 CCTGGCCATCTGCCAGCCACTCAGGTACCACGTGCTCATGAGCCACCGGCTCTGCGTGTG
 25 CTGATGGGAGCTGCCTGGGTCTCTGCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA
 TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACTTCACCTGCAAGATCCTGGCAGT
 GCTGAAGCTGGCATGCGGCAACACGTGCGTCAGCGAAGACTTCTGCTGGCGGGCTCCAT
 CCTGCTGCTGCCTGTACCCCTGGCATTATCTGCTGTCTACTTGTCTATCTTGGCCACCA
 TCTGAGGGTGCCTCGGCCGCCAGGTGCTGCAAAGCCTTCTCCACCTGCTTGGCACACCT
 30 GGCTGTAGTGTGCTTTTCTACGGCACCACATCTTTCATGTACTTGAAGCCCAAGAGTAAG
 GAAGCCACATCTCTGATGAGGTCTTCACAGTCTCTATGCCATGGTCACGACCATGTGTA
 ACCCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG
 GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

35 **AOLFR36 sequences:**

MYLVTVLRNLLSILAVSSDSHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG
 CLTQMSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLSLLDSQLHS
 WIVLQFTFFKNVEISNFVCEPSQLKLASYDSVINSIFYDNTMFGFLPISGILLSYKIVPSILRIS
 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSVAPPLRNGMVASVMYAVVTPMLNPFYIS
 40 LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

ATGTATCTGGTCACGGTGTGAGGAACCTGCTCAGCATCCTGGCTGTGAGCTCTGACTCCC
 ACCCCACACACCCATGTACTTCTTCTCTCAACCTGTGCTGGGCTGACATCGGTTTCACC
 TTGGCCACGGTTCCCAAAATGATTGTGGACATGGGGTCGCATAGCAAAGTCATCTCTTATG
 45 GGGGCTGCCTGACACAGATGTCTTCTTGGTACTTTTGCATGTATAGTAGACATGTTCTT
 GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTGCGCCTCTGCACTACCCAGTCATC
 GTGAATCCTCACCTCTGTGTCTTCTCGTTTTGGTGTCTTTTCTTAGCCTGTTGGATTCC
 CAGCTGCACAGTTGGATTGTGTTACAATTACCTTCTTCAAGAATGTGGAAATCTCTAATT
 TTGTCTGTGAGCCATCTCAACTTCTCAAGCTTGCCTCTTATGACAGCGTCATCAATAGCATA
 50 TTCATATATTTTGATAATACTATGTTTGGTTTTCTTCCCATTTTCAGGGATCCTTTTGTCTTAC
 TATAAAATTGTCCCCTCCATTCTAAGGATTTCATCATCAGATGGGAAGTACAAAGCCTTCT
 CAGCCTGTGGCTGTACCTGGCAGTTGTTTGCTTATTTATGGAACAGGCATTGGCGTGTA
 CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT
 GTGGTCACCCCATGCTGAACCTTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG
 55 CCCTGTGGAGGGTGTGCAACAAAACAGTGAATCTCATGATCTGTTCCATCCTTTTCTTG

TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCCCTAG
(SEQ ID NO: 68)

AOLFR37 sequences:

5 MEKANETSPVMGFVLLRLSAHPELEKTFVLLIMYLVILLGNGVLILVTILDSRLHTPMYFFLG
NLSFLDICFTTSSVPLVLDSTPQETISFSACAVQMALSFAMAGTECLLSMMAFDYVAICNP
LRYSVIMSKAAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVKLACADIS
INVISMEVTNVIFLGVPVLFISFSYVFIIITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTFFMYG
10 KPKSKDSMGADKEDLSKLIPLFYGVVTPMLNPIIYSLRNKDVKAAVRLLRPKGFTQ (SEQ ID
NO: 69)

ATGGAAAAAGCCAATGAGACCTCCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT
GGGCAATGGGGTCTCATCCTGGTGACCATCCTTGACTCCCGCTGCACACGCCCCATGTAC
15 TTCTTCCTAGGGAACCTCTCCTTCTGGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT
CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG
GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGATC
GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT
GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGCTGCTTCCGTGGTACACACATCCTTG
20 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCAATCAACCACTTCACTGTGAGATTCTGG
CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA
TGTGATCTTCTAGGAGTCCCGTTCTGTTTCTCTTCTCTCTATGTCTTCATCATCACCA
CCATCCTGAGGATCCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCCA
CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT
25 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAACTCATCCCCCTTTCTATG
GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

30 MYLVTVLRLNLLILAVSSDSLHTPMCFFLSNLCWADIGFTSAMVPMIVDMQSHSRVISYAGC
LTQMSFFVLFIACIEDMLLTVMAYDRFVAICHPLHYVIMNPHLGVFLVLVSFFLSLLDSQLHSW
IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFYLDSIMFGFLPISGILLSYANNVPSILRISS
SDRKSFAFSTCGSHLAVVCLFYGTGIGVYLTSVSPPPRNGVVASVMYAVVTPMLNPFIFYSLR
NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

35 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC
ACCTCCACACCCCCATGTGCTTCTTCTCCTCCTCAACCTGTGCTGGGCTGACATCGGTTTCACC
TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG
CGGGCTGCCTGACACAGATGTCTTTCTTTGTCTTTTGCATGTATAGAAGACATGCTCCTG
40 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTCACCCCTGCACTACCCAGTCATCA
TGAATCCTCACCTTGGTGTCTTCTTAGTTTTGGTGTCTTTTCTCAGCCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAATCTCCAATT
TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCTGCTGACAGTGTCATCAATAGCATA
TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTCAAGGATCCTTTTGTCTTAC
45 GCTAACAATGTCCCCTCCATTCTAAGAATTTATCATCATCAGATAGGAAGTCTAAAGCCTTCT
CCACCTGTGGCTCTCACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGTCAACACCCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT
GTGGTCAACCCCATGCTGAACCCCTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG
CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT
50 CCATCCTTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

AOLFR39 sequences:

MGVKNHSTVTEFLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVVCVISECYMLAAMACDRYVAICSPL
55 LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIUKHYFCDIVPLIKLSCSSTYIDEL

LIFVIGGFNMVATSLTIISYAFILTSILRIHKKGRCKAFSTCSSHLTAVLMFYGSLMSMYLKPAS
SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)

ATGGGTGTAAAAAACCATTCCACAGTGAAGTCTTCTTTTCTTTCAGGATTAAGTGAACAAG
5 CAGAGCTTCAGCTGCCCCCTCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG
AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCATGTACTAT
TTCCTGAGTAGTTTGTCTTTTTTAGATTTCTGCTATTCTTCTGTCATTACCCCTAAAATGCT
ATCAGGGTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTCAGCTGTTTT
TTTTCTGTGTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC
10 GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCATCATGTCCCCTAGGGTCTGTTCTCTGC
TGGTGGCTGCTGTCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGTATACT
CAGGTTGTCTTTCTGTGGATCAAACATCATTAACATTATTTCTGTGACATTGTCCCTCTTA
TTAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTTGTCAATTGGTGGATT
AACATGGTGGCCACAAGCCTAACAATCATTATTTATATGCTTTTATCCTCACCAGCATCCT
15 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTAGCACCTGTAGCTCCACCTGACA
GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCAGTTC
ACTCACCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAACTTTTAAGAAGA
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

20

AOLFR40 sequences:

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILVIRVDSHLHTPMYYFLTNLS
FIDMWFSVTVPKMLMTLVSPSGRTISFHSVAQLYFFHFLGSTBCFLYTVMSYDRYLAISSYPL
RYTNMMTGRSCALLATGTWLSGSLHSAVQTLTFHLPYCGPNQIQHYFCDAPPILKLACADTS
25 ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRIRTSEGRHRAFQTCASHCIVVLCFFGPGFLFIYL
RPGSRDALHGVVAVFYTTLTPLFNPVYTLRNKEVKKALLKLKNGSVFAQGE (SEQ ID NO:
75)

ATGTCCAACGCCACCCTACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
30 TGGACGCCCCCTCTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCTCA
CCAACCTGTCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTT
TCCACTTCTGGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACCT
35 GGCCATCAGTTACCCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG
GCCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC
ATTTGCCCTACTGTGGACCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA
GTGGCCTCGGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCT
40 GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGGACGC
CTTGCATGGGGTTGTGGCCGTTTTCTACACCACGCTGACTCCTCTTTCAACCCCTGTTGTGT
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTGAGTAT
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

45

AOLFR41 sequences:

MNPENWTQVTSFVLLGFPSHLIQFLVFLGLMVITYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN
FSFLELLLVTVVVPKMLVVILTGDHTISFVSCIHSYLYFFLGTDFLLAVMSLDRLYLAIKRPLR
YETLMNGHVCSQVLASWLAGFLWVLCPTVLMASLPFCGPNIDHFRDSWPLRLRLSCGDTH
50 LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAERRKAFSTCASHLTVVVIYGSSIFYL
IRMSEAQSKLLNKASVLSCHITPLLPNFIPTLRNDKVQQALREALGWPRLTAVMKLRVTSQRK
(SEQ ID NO: 77)

ATGAACCCTGAAAAGTGGACTCAGGTAACAAGCTTTGTCCTTCTGGGTTTCCCCAGTAGCC
55 ACCTCATACAGTTCCTGGTGTTCCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG
CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC

TTCCTGCGGAATTTCTCCTTCCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT
 TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTCAGCTGCATCATCCAGTCCCTACC
 TCTACTTCTTTCTAGGCACCACTGACTTCTTCTCTTGGCCGTCATGTCTCTGGATCGTTAC
 CTGGCAATCTGCCGACCACTCCGCTATGAGACCCTGATGAATGGCCATGTCTGTTCCCAAC
 5 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGCGGTCTTTGCCCACTGTCCTCATGGCC
 AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCGTGACAGTTGGCCCTTGCT
 CAGGCTTTCTTGTGGGGACACCCACCTGCTGAACTGGTGGCTTTTATGCTCTCTACGTTG
 GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTTATGCCTGCATTCTTGCCACTGTTCT
 CAGGGCCCCACAGCTGCTGAGCGAAGGAAAGCGTTTCCACTTGCGCCTCGCATCTTACA
 10 GTGGTGGTCATCATCTATGGCAGTTCCATCTTCTCTACATTTCGTATGTCAGAGGCTCAGTC
 CAAACTGCTCAACAAAGGTGCCTCCGTCCTGAGCTGCATCATCACACCCCTCTTGAACCCA
 TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC
 CCAGGCTCACTGCTGTGATGAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO: 78)

15

AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL
 GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFFHFIGGIKIFLLTVMAYDRYIAISQPL
 HYTLIMNQTVCALLMAASWVGGFIHSIVQIALTIQLPFCGPKLDNFYCDVPQLIKLACTDTFV
 20 LELLMVSNNGLVTLMCFLVLLGSYALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIYVY
 TRPFRITFPMDKAVSVLYTIVTPLNPAIYTLRNEKIVIMAMKKLWRRKKDPIGLEHRPLH
 (SEQ ID NO: 79)

ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT
 25 GGGAGCTTCGGTTTGTCTTCTTCACTGTTTTCTCTGCTGTGTATTTTATGACTGTAGTGGGA
 AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTTCT
 CTTGGGCAATCTTTCTTCTTCTGGACTTTTGCTACTCTTCCATCACAGCACCTAGGATGCTGG
 TTGACTTGCTCTCAGGCAACCTTACCATTTCCTTTGGTGGATGCCTGACTCAACTCTTCTTC
 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCTGTCATGGCGTATGACCGCTACA
 30 TTGCCATTTCCAGCCCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT
 ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC
 AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTTATTGTGATGTGCCTCAGCTGAT
 CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAAATGGTGTCTAACAATGGCCTG
 GTGACCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC
 35 GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT
 GGTGACCTTAATCTTTGTGCCTTGCACTACGTCTATACAAGGCCCTTTTCGGACATTCCCA
 TGGACAAGGCCGTCTGTGCTATACACAATTGTACCCCCATGCTGAATCCTGCCATCTA
 TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
 ACCCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

40

AOLFR43 sequences:

MQKPQLLVPIIATSNLGNLVHAAFYLLVGIPGLGPTIHFVLAFLPLCFMYALATLGNLTIVLIIRVE
 RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQIEFNICLAQMFLIHALSAVESAVLLA
 MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFPLPFILKWLSCQTHTVTHSFCLHQ
 45 DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRRAALKAFNTCISHLCAV
 LVFYVPLIGLSVVHRLGGPTSLHVMANTYLLLPVVNPLVYGAKTKEICSRVLCMFSSQGGK
 (SEQ ID NO: 81)

ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
 50 CAGCATACTTCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT
 TTCCCACTGTGTTTATGTATGCCTTGGCCACCCTGGGTAACTGACCATTGTCCTCATCAT
 TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCTGGCCATGCTTTCCACTATT
 GACCTAGTCTCTCTCTATCACCATGCCAAGATGGCCAGTCTTTTCTGATGGGCATCCA
 GGAGATCGAGTTCAACATTTGCCTGGCCAGATGTTCTTATCCATGCTCTGTCACGCCGTG
 55 GAGTCAGCTGCTGCTGGCCATGGCTTTGACCGCTTTGTGGCCATTGTGCCACCCATGTC
 GCCATGCTTCTGTGCTGACAGGGTGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG

GGGGTTTGTATTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCTACTGCCAAACAC
ATACTGTACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC
CAGGGTCAATGTGGTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT
TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCCCTCTCGGAGGGCA
5 GCACTCAAGGCTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC
CCTCATTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCTCCATGTGGTT
ATGGCTAATACCTACTTGTGCTACCACCTGTAGTCAACCCCTTGTCTATGGAGCCAAGA
CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID
NO: 82)

10

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVMFNGNCIVVFIVRTERSLHAPMYLFLC
MLAAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHLSAESTILLAMAFDRYVAICHP
RHA AVLNNVTVAQIGIVAVVRGSLFFFLPLLKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP
15 NVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAIFYVPLIGLS
VVHRFGNSLHPVIRVVMGDIYLLLPVINPIYGA TKQIRTRVLAMFKISCDKDLQAVGGK
(SEQ ID NO: 83)

ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA
20 AAGCCCAATTTCTGGGTGGCTTCCCCCTCCTTCCATGTATGTAGTGGCAATGTTTGGA AAC
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTC
TCTGCATGCTTGCAGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC
CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT
TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGACCGTTATGTGG
25 CCATCTGCCACCCACTGCGCCATGCTGCAGTGTCAACAATACAGTAACAGCCAGATTGG
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC
TGGCCTTCTGCCACTCCAATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA
GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC
ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTATTTTCTGATAATACGAACGGTTCTGC
30 AACTGCCCTTCCAAGTCAGAGCGGGCCAAGGCCCTTTGGAACCTGTGTGTACACATTGGTGT
GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAACAGC
CTTCATCCCATTGTGCGTGTGTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCTCAA
TCCCATCATCTATGGTGCCAAAACCAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

35

AOLFR45 sequences:

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIQADAALHEPMYLFLA
MLATIDLVLSTTLPKMLAIFWFRDQENFFACLQVMFFLHSFSIMESAVLLAMAFDRYVAICKP
LHYTTVLTGSLITKIGMAAVARA VTLMTPLPFLRRFHYCRGPVIAHCYCEHMAVVRACGDT
40 SFNNTYGIAMFVSVLDLLFVILSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVIS
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:
85)

TGGAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA
45 CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCA
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTGTGGTAGGAAT
TCCTGGTTTGGAACACCTGCATGCCTGGATCTCCATCCCTTCTGCTTTGCTTATACTCTGG
CCCTGCTAGGCAACTGTACCCTTCTCTTCATTATCCAGGCTGATGCAGCCCTCCATGAACCC
ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGGTTCTTTCTTCTACAACGCTGCC
50 CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTTCTTTGCCTGTCTGGTC
CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTT
TGACCGCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCCTGACTGGGTCCCTC
ATCACCAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCT
TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCCATGCTACTGTGAACA
55 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATTGCT
GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTTGTTATCCTGTCTTATGTCTTCATCCT

TCAGGCAGTTCTCCAGCTTGCCTCTCAGGAGGCCCGCTACAAAGCATTGGGACATGTGTG
TCTCACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG
TGTAGCCCGCCATGCTGCCCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC
CAGGATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTTCGTGAGTATGTGCT
5 CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAAATTGCAGAGT
ATCTTTGACAATTCTCTAGTATGATAAGGAAAAATGAGGTTTCATTCTCAGATCTACGA
GTCAGGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA
TTGTCAATAGACTCATCATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
10 GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID
NO: 86)

AOLFR46 sequences:

MNKHCGWHMIHTWLNIREDDSDDFKNFIGQIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHVW
15 SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLFLAMGANTLLITIQLEAS
LHQPLYLLSLLSLLDIVLCLTVIPKVLAIWFDFLRSISFPACFLQMFIMNSFLTMESCTFMVMA
YDRYVAICHPLRYPSIITDQFVARAVVFIARNAFVSLPVPMLSARLRYCAGNIKNKICSNLSVS
KLSCDDITFNQLYQFVAGWTLGSDLLIVISYFILKVVLRIKAEGAVAKALSTCGSHFILILFFS
20 TVLLVLVTNLARKRIPPDVPILLNHLHLPALNPVYGVRTKEIKQGIQNLKRL (SEQ ID NO:
87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT
GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAACCCACACT
CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTAAAGTACAC
25 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC
CAGTCTCTGAATTCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT
CTGCCCCCTCAGCCTTCTCTCCTCCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT
CCAGCTGGAGGCCTCTCTGCACCGCCCTGTACTACCTGCTCAGCCTCCTCTCCTGCTGG
ACATCGTCTCTGCCTCACCGTCATCCCCAAGGTCTGGCCATCTTCTGGTTTGACCTCAGG
30 TCGATCAGCTTCCCAGCCTGCTTCTCCTCCAGATGTTTCATCATGAACAGTTTTTTGACCATGGA
GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA
TACCCGTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA
ATGCCTTTGTTTCTTCTCTCTGTTCCCATGCTTTCTGCCAGGCTCAGATACTGTGCAGGAAAC
ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAAACTCTCTTGATGACATCA
35 CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT
ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT
GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTCAGCACAGTCC
TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCTCCAGATGTCCCCATCCT
40 GCTCAACATCCTGCACCACCTCATTCCCCCAGCTCTGAACCCATTGTTTATGGTGTGAGA
ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNITLTHPTAFLLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLLIQADAALHEPMYFLA
MLAAIDLVLSSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESA VLLAMAFDRYVAICK
45 PLHYTKVLTGSLITKIGMAAVARAVTLMTPFLPFLRCFHYCRGPVIAHCYCEHMAVVRACGD
TSFNNIYGIAMFIVVLDLLLVILSYIFILQAVLLLASQEARYKAFGTCVSHIGAILAFYTTVVIS
SVMHRVARHAAPHVHILLANFYLLFPPMVNPIYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
89)

ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCTTCTTGTTGGTGGGGATTCCAG
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG
CTTGAAACTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT
ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTCTCCTCAGCACTGCCCAAA
ATGCTTGCCATATTCTGGTTCAGGGATCGGGAGATAAACTTCTTGGCTGTCTGGCCCA
55 TGTCTTCTTCACTCCTTCTCCATCATGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA

CCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCTTCCT
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG
CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATTCTTCAG
5 GCAGTTCTACTGCTTGCCTCTCAGGAGGCCCGCTACAAGGCATTTGGGACATGTGTCTCTC
ATATAGGTGCCATCTTAGCCTTCTACACAAGTGTGGTCATCTCTCAGTCATGCACCGTGTA
GCCCCGCATGCTGCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCCACC
CATGGTCAATCCCATAATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGGA
GTATTTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

10

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTHIYVRTEHSLHEPMYIFL
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFHLSLGMESTVLLAMAFDRYVAICH
PLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLCADDDI
15 RVNVVYGLIVISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFGLSM
VHRFSKRSDSPLPVILANIYLLVPPVLPNPIVYGVKTEIRQRILRLFHVATHASEP (SEQ ID NO:
91)

ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
20 CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTTACCTTATTGCT
GTGCTAGGTAACCTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA
TGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA
GATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTT
25 GACCGCTATGTGGCCATCTGTCAACCCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG
TCACCAAAAATTGGTGTGGCTGCTGTGGTGCGGGGGGCTGCACTGATGGCACCCCTTCTGT
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCTACTGCCTACACC
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT
CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATCTTA
30 AGACTGTGTTGGGCTTGACACGTGAAGCCAGGCCAAGGCATTTGGCACTTGCCTCTCTCA
TGTGTGTGCTGTGTTTCATATTTCTATGTACCTTTTCATTGGATTGTCCATGGTGCATCGCTTA
GCAAGCGGCGTGACTCTCCGCTGCCCGTCATCTTGGCCAATATCTATCTGCTGGTTCCTCCT
GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTGACAGCGCATCCTTCGA
CTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

35

AOLFR49 sequences:

MLTFHNVCSPSSFWLTGIPGLESLSHVLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF
LCMLAIDLVLSTSTIPKLLGIFWFGACDIGLDACLGQMFLIHCFAVESGIFLAMAFDRYVAIC
NPLRHSMVLTYTVVGRGLVSLLRGVLYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALTC
40 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKTGTGCASHLCAILIFYVP
IAVSSLIHRFGQCVPPPVHTLLANFYLLIPPILNPVYAVRTKQIRESLLQPRIEMKIR (SEQ ID
NO: 93)

ATGCTCACTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG
45 GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCTTTGGCTCCATGTACCTGGTGGCTGTG
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG
TACTTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA
ACTTCTGGGAATCTTCTGGTTCCGTGCTGTGACATTGGCCTGGACGCTGCTTGGGCCAA
ATGTTCCCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCTTGCCATGGCTTTTGA
50 TCGCTACGTGGCCATCTGCAACCCACTACGTATAGCATGGTGGCTCACTTATACAGTGGTG
GGTCGTTTGGGGCTTGTCTCTCCTCCGGGGTGTCTCTACATTGGACCTCTGCCTCTGAT
GATCCGCCTGCGGCTGCCCTTTATAAAACCCATGTTATCTCCCACTCCTACTGTGAGCAC
ATGGCTGTAGTTGCCTTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT
55 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC
TTCTACCTCTGTGCCATCCTGATCTTTATGTTCCCATTGCTGTTTCTTCCCTGATTACCG

ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCCTCATTCTCCAATCCTCAATCCCATTGTCTATGCTGTTTCGCACCAAGCAGATCCGAGAGAGCCTTCTCCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

5 **AOLFR50 sequences:**

MNLDSEFFSFLKSLIMALSNSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYFLSMLAAIDL VVASSTAPKALAVLLVRAQEIGYTVCLIQMFFTHAFSSMES
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLIPFLILRLKLFQATIIGHAY
CEHMAVVKLACSETTVNRAYGLTVALLVVGDLVLAIGVSYAHILQAVLKVPNGEARLKAFST
10 CGSHVCVILVFYIPGMFSLTHRFGHHVPHHVHVLAILYRLVPPALNPLVYRVKTKQKJHQ
(SEQ ID NO: 95)

ATGAATTTGGATTCTTTTTCTCTTCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGAGGCTACCCAGCCTTCTTTTTCTGGTAGGAATCCGGGTTTAGAGGAAAGC
15 CAGCACTGGATCGCACTGCCCTGGGCATCCTTTACCTCCTTGCTCTAGTGGGCAATGTTA
CCATTCTCTCATCATCTGGATGGACCCATCCTTGCACCAATCTATGTACCTCTTCTGTCC
ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCAGTGC
TCTGGTTCGTGCCCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTCACCCAT
GCATTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
20 TTTGTCAACCCCTTGCACCATTCCACAATCCTGCATCCAGGGGTCATAGGGCACATCGGAAT
GGTGGTGTCTGGTGGGGGATTACTACTCCTCATCCCTTCTCATTCTGTTGCGAAAACCTT
ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC
TTGCCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT
TGGGCTGGATGTCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGAAG
25 GTACCAGGAAATGAGGCCGACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTTGTGTCA
TCCTGGTCTTCTATATCCCGGGAATGTTCTCCTTCTCCTCACTACCGCTTTGGTCATCATGTA
CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACTCAATCC
TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

30 **AOLFR51 sequences:**

MCQQLRDCILLIHLICNRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAM
YIALLGNTIIVTAIWMDSTRHEPMYCFLCVLAAVDIVMASSVVPKMVSIFCSGDSISFSACFTQ
MFFVHLATAVETGLLLTMAFDYVAICKPLHYKRILTPQVMLGMSMAITIRAIATPLSWMVS
HLPFCGSNVVVHSYCEHIALARLACADPVPSLSYSLIGSSLMVGSDVAFIAASYILKAVFGLSS
35 KTAQLKALSTCGSHVGVMAlyLPGMASIYAAWLGQDVVPLHTQVLLADLYVIIPATLNPIY
GMRTKQLRERIWSYLMHVLFDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
40 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
45 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCAGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
50 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAAGCATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCCAAGTCTGCTC
TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAACTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
55 CTGGGTTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAMYITALLGNTLIVTAIWMSTRHEPMY
 CFLCVLAADVIMASSVVPKMVSIFCSGDSISFSACFTQMFFVHLATAVETGLLLTMAFDRIYV
 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLPCGNSNVVHSYCKHIALAR
 5 LACADPVPSSLYSLIGSSLMVGSDVAFLAASYILILRAVFDLSSKTAQLKALSTCGSHVGVMA
 YLPGMASITYAAWLGQDIVPLHTQVLLADLYVIIIPATLNPIYGMRTKQLLEGIWSYLMHFDFH
 SNLGS (SEQ ID NO: 99)

ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCTCCTTGTGGGTA
 10 TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC
 AGCCCTGTTAGGAAACACCCTCATCGTGAAGTCAATCTGGATGGATTCCACTCGGCATGAG
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC
 ACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG
 15 CTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCTCA
 AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTCATGACTCCACTG
 AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA
 GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG
 ATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT
 20 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAGCACATGT
 GGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG
 CCTGGTTGGGGCAGGATATAGTGCCCTTGACACCCAAGTGCTGCTAGCTGACCTGTACGT
 GATCATCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG
 GGAATATGGAGTTATCTGATGCACTTCTCTTGACCACTCCAACCTGGGTTTCATGA (SEQ
 25 ID NO: 100)

AOLFR54 sequences:

MSDSNLSDNHLPDTFFLTGIPGLEAAHFVIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
 LFLCLLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFVHSIYALESSILLAMAFDRYVA
 30 ICNPLRYTTILNHAIVIGRIGFVGLFRSVAIVSPFILLRRLPYCGHRVMTHTYCEHMGRIARLACA
 NITVNIVYGLTVALLAMGLDSILIAISYGFILHAVFHLPSHDAQHKALSTCGSHIGIILVFYIPAFF
 SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
 NO: 101)

ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
 35 CAGGGCTGGAGGCTGCCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC
 ACTGGTTGGAAATGCTGCCCTCATCCTGGTCAATTGCCATGGACAATGCTCTTCATGCACCT
 ATGTACCTCTTCTCTGCCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC
 CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCTTTGGTGGATGCCTGGCC
 40 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCTCGATTCTACTTGCCATGGCCTT
 TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTTCTCAACCATGCTGTC
 ATAGGCAGAAATGGCTTTGTTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT
 CTTGCTGAGGCGACTCCCCTACTGTGGTCACCGTGTCATGACACACATACTGTGAGCAT
 ATGGGCATCGCCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG
 45 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCTATGGCTTTATCCTC
 CATGCAGTCTTTACCTTCCATCTCATGATGCCAGCACAAAGCTCTGAGTACCTGTGGCT
 CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCTCACCCACCGC
 TTTGGTCAACACGAAGTCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG
 TGCCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTGGGAGTCGACT
 50 TCTAAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVTYMFYLHWTMEKSNNSTLFILLGFSQNKNEIIVLCFVLFVFCYIAIWMGNLLIMISITCTQ
 LIHQPMYFFLNYLSLDLCYTSTVTPKLMVDLLAERKTISYNNCMIQLFTTHFFGGIEIFILTM
 55 AYDRYVAICKPLHYTIIMSROKCNTHIVCCTGGFIHSASQFLITIFVPCGPNEIDHYFCDVYPL
 KLACSNHIMIGLLVIANSGLIALVTFVLLSYVFILYTIRAYSAERRSKALATCSSHVTVVVLFF

APALFIYIRPVTTFSEDKV FALFYTHAPMFNPLIYTLRNTMKNAMRKVWCCQILLKRNQLF
(SEQ ID NO: 103)

5 ATGTCATTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAGCAATAATA
GCACTTTGTTTATTCTCTTGGGGTTTTCCCAAAATAAGAACATTGAAGTCCTCTGCTTTGTA
TTATTTTTGTTTTGCTACATTGCTATTTGGATGGGAACTTACTCATAATGATTCTATCAC
GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCTCAATTACCTCTCACTCTCCGACC
TTTGCTACACATCCACAGTGACCCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC
CATTTCCTATAATAACTGTATGATACAACCTCTTACCACCCATTTTTTTGGAGGCATAGAGA
10 TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCCTGCACTA
CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTACTGGGGGA
TTTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCATTTTGTGGCCCAATGA
GATAGTCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
TGATAGGTCTCTTAGTCATTGTCTAATTCAGGCTTAATTGCTTTGGTGACATTGTGTCTTG
15 TTGTTGTCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA
AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCTGTTTTTGTCTCTGCATTG
TTCATTTACATTAGACCGGTCACAACATTCTCAGAAGATAAAGTGTTTGCCTTTTTTATAC
CATATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
GCCATGAGGAAAGTGTTGGTGTGTCAAATACTCCTGAAAAGAAATCACTTTTCTGA (SEQ
20 ID NO: 104)

AOLFR58 sequences:

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQPNVQEI VVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACCSSVI
25 TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMDLYPLELACTDTHIFGLMVVINS
FICINFSLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYILNPLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

30 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACTTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAATTTCTTTGTCTTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCTCTGGGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTCTC
35 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTGGGCTTCTGTCTTCTGGA
TGCGTGCTTCTCATCTGTCTATCAACCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
40 GGCCCTCTGCATTCCATGATACAAATTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
45 TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 106)

AOLFR59 sequences:

MGDWNNSDAVEPIFILRGFPGLLEYVHSWLSILFCLAYLVAFMGNVTILSVIWIESSLHQPMYYFI
SILAVNDLGMSTLPTMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
PLHYPTILNSVIGKIGLACLLRSLGVVLPPLLLRHYHYCHGNALSHAFCLHQDVLRLSCTDA
RTNSIYGLCVVIATLGVDISIFILLSYVLILNTVLDIASREEQLKALNTCVSHICVVLFFVPVIGVS
55 MVHRFGKHLSPIVHILMADIYLLPVLNPIVYSVRTKQIRLGILHKFVLRRLF (SEQ ID NO:
107)

ATGGGAGACTGGAATAACAGTGTATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCTTG
 GACTGGAGTATGTTTCATTCTTGGCTCTCCATCCTCTTGTCTTGCATATTTGGTAGCATTT
 ATGGGTAAATGTTACCATCCTGTCTGTTCATTGGATAGAATCCTCTCTCCATCAGCCCATGTA
 5 TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCACCA
 TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT
 GTTCTTCATCCACACATTCACATTCCTGGAGTCCCTCAGTGTTGCTGGCCATGGCCTTTGACC
 GTTTTGTGCTATCTGCCATCCACTGCACTACCCACCATCCTACCAACAGTGTAATTGGC
 AAAATTTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTACTTCCACACCTTTGCTACT
 10 GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCTTCTGTTTGCACCAGGAT
 GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
 TTGCCACACTAGGTGTGGATTCAATCTTCATACTTCTTTCTTATGTTCTGATTCTTAATACT
 GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCATATA
 TCTGTGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG
 15 AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT
 CCTTAACCCTATTGTCTATAGTGTGAGAACAAGCAGATTCTGTCTAGGAATTCTCCACAAG
 TTTGTCCTAAGGAGGAGGTTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

20 MFLPNDTQFHPSSFLLGLPGLETLHIWIGFPFCVYMIALIGNFTILLVKTDSLSLHQPMPFYFLA
 MLATTDVGLSTATIPKMLGIFWINLRGHFEACLTQMFFIHNFTLMESAFLVAMAYDSYVAICN
 PLQYSAILTNKVVSIGLVFVRALIFVIPSILLILRPFNGNHVIPHTYCEHMGHLASCAKINI
 IYGLCAICNLVFDITVIALSYVHILCAVFRLPHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
 FGRNVPRYIHILLANLYVVPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF
 25 (SEQ ID NO: 109)

ATGTTCCCTTCCCAATGACACCCAGTTTCACCCCTCCTCCTTCCCTGTTGCTGGGGATCCCAGG
 ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC
 ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCATGT
 30 TCTACTTCCCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA
 GATGCTTGGAATCTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG
 ATGTTTTTTTATCCACAACCTTCACACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG
 ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTACCAACAAGGTTGT
 TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTCGTCATTCCCTCTATACTTC
 35 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCCCCACACCTACTGTGAGCACAT
 GGGTCTTGTCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTTATGGTTTATGTGCCA
 TTTGTAATCTGGTGTGTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATCTTTGTGCT
 GTTTTCCGTCTTCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTCACATGT
 GTGTGTAATCCTTGCTTCTATACACCAGCCCTCTTTCTTTTATGACTCATTGCTTTGGCC
 40 GAAATGTGCCCCGCTATATCCATATACTCTAGCCAATCTCTATGTTGTGGTGCCACCAAT
 GCTCAATCCTGTCTATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT
 ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA
 (SEQ ID NO: 110)

AOLFR61 sequences:

45 MSINTSYVEITTFVLVGMPLGLEIAHIWISIPICSMYLIAILNGTTLFIKTEPSLHGPMYYFLSML
 AMSDLGLSLSSLPTVLSIFLNPETSSSACFAQEFFFHGFVLESSVLLIMSFDRFLAIHNPLRYT
 SILTTVRVAQIGIVFSFKSMMLVLPFPFTLRSRKYCKKNQLSHSYCLHQDVMKLACSDNRIDVTY
 GFFGALCLMVDFILIAVSYTLILKTVPGIASKKEBKALNTCVSHICAVIIFYLPINLAVVHRFAG
 50 HVSPLINVLMANVLLLVPPLMKPIVYCVKTKQIRVRVAVKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
 CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCCATGT
 55 ACTATTTTCTTTCCATGTTGGCTATGTGAGACTTGGGTTTGTCTTATCATCTCTGCCCACT
 GTGTTAAGCATCTTCTGTTCAATGCCCTGAAACTTCTTCTAGTGCTGCTTTGCCCAGGA

ATTCTTCATTTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA
 GATTCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 5 TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
 TGTGATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
 ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTACACATC
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCG
 10 GCATGCTCTCTCCCTCATTAATGTTCTCATGGCAAATGTTCTCTACTTGTACCTCCGCTGA
 TGAAACCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
 GTGTCAATGGAAGATTAA (SEQ ID NO: 112)

AOLFR62 sequences:

MFYHNKSIHPVTFLLIGIPGLEDFHFWISGPFCSVYLVALLGNATILLVIKVEQTLREPMFYFL
 15 AILSTIDLALSATSVPRMLGIFWDAHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC
 APLHYATILTSVLVIGISMCTVIRPVLLTLPVYLIYRLPFCQAHIAHSYCEHMGIAKLSCGNIRI
 NGIYGLFVVSFFVLNLVLIGISYVYILRAVFLRPSHDAQLKALSTCGAHVGVICVFYIPSVFSFLT
 HRFHQIPGYIHLVANLYLIPPSLNPIHYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

20 ATGTTTTATCACAACAAGAGCATATTTACCCAGTCACATTTTTCTCATTGGAATCCCAGG
 TCTGGAAGACTTCCACATGTGGATCTCCGGGCTTTCTGCTCTGTTTACCTTGTGGCTTTGC
 TGGGCAATGCCACCATCTGCTAGTCATCAAGGTAGAAGAGACTCTCCGGGAGCCCATGTT
 CTACTTCTGGCCATTCTTTCCACTATTGATTTGGCCCTTTCTGCAACCTCTGTGCCTCGCA
 TGCTGGGTATCTTCTGGTTTGATGCTCAGGAGATTAAGTATGGAGCTTGTGTGGCCCAGAT
 25 GTTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC
 CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTGGT
 GGGCATTAGCATGTGCATTGTAATTCGTCCCGTTTTACTTACACTTCCCATGGTCTATCTTA
 TCTACCGCTACCTTTTGTGAGGCTCACATAATAGCCATTCTACTGTGAGCAGATGGG
 CATTGCAAAAATTGTCTGTGGAAACATTCGTATCAATGGTATCTATGGGCTTTTTGTAGTTT
 30 CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC
 TTCCGCCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG
 GAGTCATCTGTGTTTTCTATATCCCTCAGTCTTCTCTTCTTACTCATCGATTTGGACAC
 CAAATACCAGGTTACATTACATTCTTGTGCAATCTCTATTTGATTATCCCACCTCTCT
 CAACCCCATCATTTATGGGGTGAGGACAAACAGATTGAGAGCGAGTGCTCTATGTTTTT
 35 ACTAAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSIINTSYVEITTFVLVGMPLGLEYAHIWISIPICSMYLLAILGNGTILFIKTEPSLHEPMYYFLSML
 AMSDLGLSLSSLPTVLSIFLNAPEISSNACFAQEFFFHGFVLESSVLLIMSFDRFLAIHNPLRYTS
 40 ILTTRVVAQIGIVFSFKSMLLVLPFFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
 GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPINLAVVHRFAR
 HVSPLINVLMANVLLLVPPLTNPIVYCVKTKQIRVRVAKLCQRKI (SEQ ID NO: 115)

45 ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
 CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCCATGT
 ACTATTTTCTTTCCATGTTGGCTATGTGAGACTTGGGTTTGTCTTATCATCTCTGCCCCT
 GTGTTAAGCATCTTCTGTTCAATGCTCCTGAAATTTCAATCCAATGCCTGCTTTGCCAGGA
 ATTCTTCATTTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA
 50 GATTCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
 TGTGATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
 55 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTACACATC
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG

GCATGTCTCTCCCCTCATTAAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGACGAACCCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATTGTGTCAACGGAAGATTTAA (SEQ ID NO: 116)

5 **AOLFR64 sequences:**

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTIVILGNLTILHVICTDATLHGPMYYFLGMLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPLHDSTVLTPACIVKMGSLSSVLRSAALLPLPFLKRFQYCHSHVLAHAYCLHLEIMKLACSSIIVNHIYGLFVVACTVGVDLLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLVHFRGEHLPRVVHLFMSYVYLLVPPLMNPPIYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCTGACGGGCTTCCAAGGTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATCTTGGGGAACCTCACCATTCTCCACGTCATTTGTACTGATGCCACTCTCCATGGACCCATGTACTATTCTTGGGCATGCTAGCTGTACAGACTTAGGCCTTTGCCTTTCCACACTGCCCACTGTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGCTCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGACCGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCAACCGTCTGACACCTGCATGTATTGTCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCCTTGCCATTCTCTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTACCTGGAGATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTGGCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTCTCTCATACGCCCTCATCTTCGCACCGTGCTCAGCATTGCCTCCACAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCATATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTTGTGCATCGCTTTGGTGAACATCTGCCCCGCGTTGTACACCTCTTCATGTCCTATGTGTATCTGCTGGTACCACCCCTTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAAGAA GTTTCAGTTTATAAAGTCACCTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

30 **AOLFR65 sequences:**

MAGRMSTSNHTQFHPSSFLLLGIPGLEDVHIWIGVPFFVYLVALLGNTALLFVIQTEQSLHEPMYYFLAMLDSIDLGLSTATIPKMLGIFWFKKEISFGGCLSHMFFIHFHTAMESIVLVAMAFDRYIAICKPLRYTMILTSKIIISLIAGIAVLRSLYMVVPLVFLLLRPFCHRIIPHTYCEHMGRIARLACASIKVNIRFGLGNISLLLLDVILIISYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFLTHRFHGNIPQYIHIILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCTACTGCTGGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTTCTTTGTGTATCTGTGTGCACTCCTGGGAAACACTGCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCCATGAGCCTATGTACTACTTCCCTGGCCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGCCACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTTGGAGGCTGCCTTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGCCATGGCCTTTGACCGCTACATTGCCATTTGCAAACCTCTTCGGTACACCATGATCCTCACCA GCAAAATCATCAGCCTCATTGCAGGCATTGCTGTCTGAGGAGCCTGTACATGGTTGTTCCACTGGTGTCTTCTCCTTCTGAGGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATTGTGAGCACATGGGCATTGCCCCTGTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGGCCTTGGAACATATCTCTCTTGTACTGGATGTTATCCTTATTATCTCTCTATGTACAGGATCCTGTATGCTGTCTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGTCTCATATTGGTGTATCTTAGCCCTTTTACACCAGCATTTTTTCACTTCTTGACACATCGTTTTGGCCATAATATCCACAGTATATACATATTATATTAGCCAACCTGTATGTGGTTGTCCACAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTTCGAGAGAGAGTGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

AOLFR66 sequences:

55 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFLALLSFTDVLMTSTLPTLNTLFIWNLKEIDFKACLAQMFFVHTFTGMESGVLMMLMALDHCVAI

CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLT KRLPYCKGNVIPHTYCDHMSVAKJSCGN
VRVNAIYGLIVALLIGGFDILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF
TFFTHHFGGHTIPLHIHUMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ
ID NO: 121)

5

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTCATCCTAAATGGCATCCCTG
GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTGCTATT
ACAGGGAACCTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT
ATGTCTTCCTTGCCCTTCTTTCCTTCACAGATGTGCTCATGTGCACCAGCACCCCTTCCCAAC
10 ACTCTCTTCATATTGTGGTTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCAGAT
GTTCTTTGTGCACACCTTCACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC
TAAAGCTGGGTTCCTCACTTTTCTTAGGGGTGTGATGCTTGTATCCCTTCCACTTTCTCTCA
CCAAGCGCCTTCCATACTGCAAGGGCAACGTACATCCCCACACCTACTGTGACCACATGTC
15 TGTGGCCAAGATATCTTGTGGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC
CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC
AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACTGCCCCAC
TTCTGTGCCATAGTCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCATTTTGG
GGGACACACCATTCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC
20 CCACAATGAACCCTATTGTGTATGGGGTGAAAACAGGCAGGTACGAGAAAGTGTCAATTA
GGTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIA VVGNCGLICLISHEEALHRPMYYFLA
25 LLSFTDVTLCITMVPNMLCIFWNLKEIDFNACLAQMFFVHMLTGMESGVMLMLALDRYVAI
CYPLRYATILTNPVIAKAGLATFLRNVMILIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
FKVNAIYGLMVALLIGVFDICCSVSYTMILQAVMSLSSADARHKAFTSTSHMCSIVITYVAAP
FTFFTHRFVGHNPNIHIIIVANLYLLLPTMNPVYGVKTKQIQEGVIKFLLDGKVSFTYDK
(SEQ ID NO: 123)

30

ATGTCTGGGGACAACAGCTCCAGCCTGACCCAGGATTCTTTATCTTGAATGGCGTTCTCTG
GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC
GTGGGGAACCTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACGGGCCATGT
ACTACTTCCTGGCCCTGCTCTCCTTCACTGATGTCACCTTGTGCACCACCATGGTACCTAAT
35 ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCAGAG
TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA
CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG
CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCCATTCCTCTCCTC
ACCAAGCGCCTGCCCTATTGCCGGGGGAACCTTCATCCCCACACCTACTGTGACCATATGT
40 CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC
TCTCTGATTGGTGTGTTTGATATCTGCTGATCTCTGTATCTTACACTATGATTTTGCAGG
CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA
CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTTGT
AGGACACAATATCCCAAACCACATACACATCATCGTGGCCAACCTTTATCTGCTACTGCCT
45 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTGAGGAAGGTGTAATTA
AATTTTTACTTGAGACAAGGTTAGTTTACCTATGACAAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSQHWLSLPLSLLFLLAVGANTTLLMTIWLEASLHQPL
50 YYLLSLLSLLDIVLCLTVIPKVLTFWFDLRPISFPACFLQMYIMNCF LAMESCTFMVMAYDRY
VAICHPLRYPSTHDFVKAAMFILTRNVMLTLPILSAQLRYCGRNVIENCICANMSVSRSLC
DDVTINHL YQFAGGWTLGSDLILFLSYTFILRAVLR LKAEGAVAKALSTCGSHFMLILFFSTIL
LVFVLTHVAKKKVSPDVPVLLNVLHHVIPAALNPIYGVRTQEI KQGMQRLLKKGC (SEQ ID
NO: 125)

55

ATGACAACACACCGAAATGACACCCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
 TTGTCAGATCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCTCAGCCTCCTTTTCTCTTG
 GCCGTAGGGGCCAACACACCCCTCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC
 CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC
 5 CCCAAGGTCCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCTGCCTGCTTCCT
 CCAGATGTACATCATGAATTGTTTCTAGCCATGGAGTCTTGACATTCATGGTCATGGCC
 TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATCACTGATCACTT
 TGTAAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCATCCCC
 ATCCTTTTCAACACAACCTCCGTTATTTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA
 10 ATATGTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCTCTACACCTTCATTCT
 GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG
 CTCCCACTTCATGCTCATCCTCTTCTTTCAGCACCATCCTTCTGGTTTTTGTCTCACACATGT
 GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT
 15 CCTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCAAGAAATTAAGCAGGGAATG
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

MSYSIYKSTVNIPLSHGVVHSFCHNMNCFMHIFKVLDFNMKNVTEVTLFVLKGFTDNLELQ
 20 TIFFFLFLAIYFLTLMGNLGLLVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
 KVISFLGCVAVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVSMSPRVYVPLINASYVAGI
 LHATHITVATFSLFCGANEIRRVFCDDIPLLAISYSDHTNQLLLFYFVGSIELVTILIVLISYGLIL
 LAILKMYSAEGRRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHDMIVSIFYTIVIPLLNPV
 IYSLRNKDVKDSMKKMFCKNQVINKVYFHTKK (SEQ ID NO: 127)

25 ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCCTTGAGTCATGGTGTGTTTCATT
 CTTTTTGTCAATATGAACTGTAACCTTATGCATATCTTCAAGTTTGTCTAGATTTCAAC
 ATGAAGAATGTCACTGAAGTTACCTTATTTGACTGAAGGGCTTCACAGACAATCTTGAAC
 TGCAGACTATCTTCTTCTCCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTTA
 30 GGAGTGATTTTAGTGGTCAATTAGGGATTTCCAGCTCCACAAACCCATGTACTATTTCTGA
 GTATGTTGCTTCTGTGGATGCCTGCTATTCCCTCAGTTATTACCCCAAATATGTTAGTAGAT
 TTTACGACAAAGAATAAAGTCATTTTCTTGGATGTGTAGCACAGGTGTTTCTTGCTT
 GTAGTTTTGGAACACAGAATGCTTTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC
 CATCTACAACCCCTCTCCTGTATTCAGTGAGCATGTCACCCAGAGTCTACATGCCACTCATC
 35 AATGCTTCCTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGCCT
 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTGTGATATCCCTCCTCTCCTTGCTA
 TTTCTTATTCTGACACTCACACAAACAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG
 CTGGCTCACTATCCTGATTGTTCTGATCTCCTATGGTTTGATTCTGTTGGCCACTGAAGAT
 GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACTAAGTGAAGT
 40 GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTTCAGCTATGCTTCG
 GACCATGACATGATAGTGTCAATATTTTACACCATTGTGATTCCCTTGCTGAATCCCGTCAT
 CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA
 GGTATCAATAAAGTATATTTTCACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

45 MDSTFTGYNLVNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLFFAI
 YLFTLIGNLGLVVLVIEDSWLHNPMMYYFLSVLSFLDACYSTVVPKMLVNFLAKNKSISFIGCA
 TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVSMSPRVYVPLITASVYAGILHATHIVA
 TFSLSFCGSNEIRHVFCDDIPLLAISCSDDHTNQLLLFYFVGSIEIVTILIVLISCDFILLILKMHS
 50 KGRQKAFSTCGSHLTGVTIYHGTLVSVMRPSYASDHDIIVSIFYTIVIPKLNPIIYSLRNKEVK
 KAVKKMLKL VYK (SEQ ID NO: 129)

ATGGACTCCACTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAAACTGAAATGGACA
 AGTTGTCATCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA
 55 TGTTTATATTGACAGGCTTCACAGATGATTTTGAGCTGCAAGTCTTCTATTTTACTATTT
 TTTGCAATCTATCTCTTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG

ATTCCTGGCTCCACAACCCCATGTATTATTTCTTAGTGTTTATCATTCCTTGGATGCTTGC
 TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGGCAAAAAATAAATCCATTT
 CATTTATCGGATGTGCAACACAGATGCTTCTTTTGTACTTTTGGAACTACAGAATGTTTT
 CTCTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCTCTCCTGTATTCACT
 5 GAGCATGTCACCCAGAGTCTATGTGCCACTCATCACTGCTTCTACGTTGCTGGCATTTTAC
 ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCTTCTGTGGATCCAATGAAATTAG
 GCATGTCTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC
 AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTCACTATCCTGATTGTCTCATT
 TCCTGTGATTTCATTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG
 10 CCTTCTCTACATGTGGCTCTCACCTAACTGGAGTGACAATTTATCATGGAACAATTCTCGTC
 AGTTATATGAGACCAAGTTCCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTTT
 ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA
 AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

15 **AOLFR71 sequences:**

MGRNRNTNVPDFILTGLSDSEEVQMALFILLLIYLLITMLGNVGMILIRLDLQLHTPMYFFLTH
 LSFIDLSTVITPKTLANLLTSNYISFMGCFAQMFFVFLGAAECFLSSMAYDRYVAICSPRLY
 PVIMSKRLCCALVTGPYVISFNSFVNVMWSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI
 MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTFYGTMIFTYKPRK
 20 SYSLGRDQVASVFYTVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG
 AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC
 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATTTTT
 25 TCCTTACTCACTTGTCAATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAAACCTTA
 GCGAACTTACTGACTTCCAATATATTTCTTTCATGGGCTGCTTTGCCAGATGTTCTTTTT
 TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCATCAATGGCCTATGATCGCTACGTAG
 CTATCTGCAGTCCCTTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC
 ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC
 30 TGCATTTCTGCGACTCAAATGTAGTTCTGCTCACTTTTTCTGCGACACGTCTCCAATTTAGCT
 CTGTCCTGCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC
 TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTTACCATCCTGAAA
 ATTAATCCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG
 TCACCATCTTTTATGGAAGTATGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCTTTG
 35 GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT
 TTATAGTCTTAGAAACAAAGAAGTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
 GGACTCCAGGTAA (SEQ ID NO: 132)

AOLFR72 sequences:

40 MAPENFTRVTEFILTVSSCPQLPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL
 ALINLGNSTVIAPKMLINFLVKKKTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
 YMVVSRRLCLLLVSLTYLYGFSTAIVVSSYVFSYCSSNIINHFCYDNVPLLALSCSDTYLPE
 TVVFISAATNVVGLIVLVSYFNIVLSILKICSEGRKKAFTSCASHMMAVTIFYGTLFFMYVQP
 RSNHSLDTDDKMASVFYTLVIPMLNPLIYSLRNKDVKLTALQRFMTNLCYSFKTM (SEQ ID NO:
 45 133)

ATGGCTCCTGAAAATTTACCAGGGTCACTGAGTTTATTCTTACAGGTGCTCTAGCTGTC
 CAGAGCTCCAGATTCCCCTCTTCTGGTCTTTCTGGTGCTCTATGGGCTGACCATGGCAGG
 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCCATGACTTTT
 50 TCCTGCAACATCTGGCTCTCATTAACTCTTGGTAACTCTACTGTCATTGCCCTAAAATGCTG
 ATTAACTTTTAGTAAAGAAGAAAACCTCATTCTATGAATGTGCCACCAACTGGGAG
 GGTTCTTGTCTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT
 GTGGCTATTTGTAACCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCTCCTGCT
 GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT
 55 CTGTGCTTATTGCTCTTCTAATAATAATCAATCATTTTACTGTGATAATGTTCCCTCTGTTA
 GCATTATCTTGCTCTGATACCTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA

ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA
 AAAATATGTTTCATCAGAAGGAAGGAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG
 CAGTCACAATTTTTATGGGACATTGCTATTCATGTATGTGCAGCCCCGAAGTAACCATTC
 ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCCTATGCTGAAT
 5 CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA
 AATCTGTGCTATTCCTTTAAACAATGTAA (SEQ ID NO: 134)

AOLFR73 sequences:

MNHVVKHNHTAVTKVTEFILMGITDNPGLQAPLFLIYLVTVIGNLGMVILTYLDSKLHTP
 10 MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIISSELFILSAMA YDRYV
 AICKPLLYVHMAEKVLWVLVVPYLYSTFVSLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
 NELELILIFSGCNLLFSLIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFIYL
 QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

15 ATGAATCATGTGGTAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA
 TGGGGATTACAGACAACCTGGGCTGCAGGCTCCACTGTTGGACTCTTCCTCATCATATA
 TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA
 CACACCCCATGTACTTTTTCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT
 CATTGCCCCGAAGATGTTAGTAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG
 20 TATGCCACTCAGCTAGCAATCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT
 TCTCACAATTAAGTTATTTAACTGTCTTCTGTGGCTCAAACATAATCAGCTATTTTTACT
 GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT
 25 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
 TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC
 TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTTACTTGCA
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCTGTTG
 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAGATGCTCTAA
 30 AGAGAACTTTAACCAATCGATTCAAAATCCCATTAA (SEQ ID NO: 136)

AOLFR74 sequences:

MEQHNLTTVNEFILTGITDIAELQAPLFLFMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
 LAFMDLGYSTTVGPKMLVNFVVDKNIISYFYCATQLAFFLVFIGSELFILSAMS YDLYVAICNPL
 35 LYTVIMSRRVCQVLVAIPYLYCTFISLLVTIKIFTLFCGYNVISHFYCDLPLPLLCNTHIEILI
 ILFAADLISLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMYVQPKSSH
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

40 ATGGAACAACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC
 GCTGAGCTGCAGGCACCATTATTTGCATTGTTCCCTCATGATCTATGTGATCTCAGTGATGG
 GCAATTTGGGCATGATTGTCCTACCAAGTTGGACTCCAGGTTGCAAACCCCTATGTAATT
 TTTTCTCAGACATCTGGCTTTCATGGATCTTGGTTATTCAACAACGTGGGACCCAAAATG
 TTAGTAAATTTGTTGTGGATAAGAATATAATTTCTTATTATTTTGTGCAACACAGCTAGC
 TTTCTTTCTTGTGTTTATTGGTAGTGAACCTTTTATTCTCTCAGCCATGTCCTACGACCTCT
 45 ATGTGGCCATCTGTAACCCTCTGCTATACACAGTAATCATGTACGAAGGGTATGTCAGGT
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCATTTCTTCTTAGTCACCATAAAGATTT
 TTACTTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGTCTCCCTTTG
 TTACCTTTGCTTTGTTCAAATACACATGAAATGAAATGATAATTCTGATCTTTGCAGCTAT
 TGATTTGATTTTCATCTCTTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT
 50 CAGGATGAATCTGCTGGCAGACAAAAGGCTTTTTCTACCTGTGGAGCCACCTGACAGTG
 GTCATAGTGTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCTT
 TGACACTGATAAAGTGGCTTCCATATTTTACACCCTGGTTATCCCCATGTTGAATCCCTTGA
 TCTATAGTTTACGAAACAAAGATGTAAATATGCCCTACGAAGGACATGGAATAACTTATG
 TAATATTTTTGTTTAA (SEQ ID NO: 138)

55

AOLFR75 sequences:

MEGKNQTNISEFLLGFSSWQQQVLLFALFLCLYLTLGLFGNLLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVPKMLLNQQTQTISYPGCLAQMYFCMMFANMDNFLTVMAYDRYVAI
 CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMMAHLHFCDNVIHHFFCDINSLPLSCSD
 5 TSLNQLSVLATVGLIFVPSVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFYSLRNNELKGTLLKTLSPGAVAHACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC
 10 AACACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTCTATTTAACAGGGCTGTTTGGA
 AACTTACTCATCTTGCTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT
 CCTTGCCAATCTGTCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT
 CTGTATGATGTTTGCCAATATGGACAATTTTCTTCTCACAGTGATGGCATATGACCGTTAC
 15 GTGGCCATCTGTCAACCTTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT
 GGTAGCTGCACCTTGGGTCAATTGCCATTTTGAACCCTCTCTTGCACACTCTTATGATGGCCC
 ATCTGCACCTTCTGCTCTGATAATGTTATCCACCATTCTTCTGTGATATCAACTCTCTCCTC
 CCTCTGTCTGTTCGACACCACTTAATCAGTTGAGTGTTCTGGCTACGGTGGGGCTGA
 TCTTTGTGGTACCTTCAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG
 20 AAAGTCCCTTCTGCCCAAGGAAAACCTCAAGGCTTTCTCTACCTGTGGATCTCACCTTGCCTT
 GGTCATTCTTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCCTTATCCAATCACTCT
 ACTGAAAAAGACTCAGCCGCATCAGTCATTTTATGGTTGTAGCACTGTGTTGAATCCAT
 TCATTTACAGTTTAAGAAACAATGAAGTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC
 CGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA
 25 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

MENNTVESEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMIIILLDSHLHTPMYFFLSNLSLA
 GIGYSSAVTPKVLTLGLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY
 30 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL
 VLISFNVFFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM
 DTDKIASVFYTMIPMLSPIVYTLRNKDVKNAMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA
 35 CTACAGGTTCCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTGACTGGGAACCT
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTTCTCA
 GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTAACTGG
 GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTGT
 GCAGTCTTTGCCACTGTGGAAAATTACCTCTTGTCTCAATGGCCTATGACCGCTACGCAG
 40 CAGTGTGTAACCCCTACATTATACCACCACCATGACAACACGTGTGTGTGCTTGTCTGGC
 TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTCGCC
 TCTCTTCTGCATGTCCAATGTGATTTCATCACTTTTTCTGTGACAAACCAGCAGTCATTACT
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTCTTATATCAAGTTTTAATGT
 CTTTTTTGCACTTCTTGTACCTTGATTTCCTATCTGTTTCATATTGATCACCACTCTTAAGAG
 45 GCACACAGGTAAGGGATACCAGAAGCCTTTATCTACCTGTGGTTCTCACCTCATTGCCATT
 TTCTTATTTTATATAACTGTCATCATCATGTACATACGACCAAGTCCAGTCATTCCATGGA
 CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT
 ATACCTGAGGAACAAAGACGTGAAGAATGCATTCATGAAGGTTGTTGAGAAGGCAAAAT
 ATTCTCTAGATTCAGTCTTTAA (SEQ ID NO: 142)

50

AOLFR77 sequences:

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTLMGVAEGVLLVLMSYDRYVAVC
 QPLQYPVLMRRQVCLMMGSSWVVGVLNASIQTSITLHFPYCASRVDHFFCEVPALLKLSCA
 55 DTCAYEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEARHKAVTTCSSHITVVGFLFYGA

AVFMYMVP CAYHSPQQDNVVS LFYSLV TPTLNPLIYSLRNPEVWMA LKVLSRAGLRQMC
(SEQ ID NO: 143)

5 ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT
CAGGATCACGCCAGCTCCTCTTCTCCCTGGTGGCTGTCATGTTTGT CATAGGCCTTCTGGGC
AACACCGTTCTTCTCTTCTTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTACTTCCT
GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA
TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT
TCCTCACACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCCTCATGTCTTATGACCGTTA
10 TGTGTCTGTGTGCCAGCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG
ATGATGGGCTCCTCCTGGGTGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATCACCC
TGCAATTTCCCTACTGTGCCTCCCGTATGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA
CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC
TGATCCTAATGCTCCCTCTTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT
15 CTAAGACTGCGCTCAGAGGAGGCCAGACACAAGGCTGTCAACCTGCTCCTCGCACATCA
CGGTAGTGGGCTCTTTTATGGTGCCGCGTGTTCATGTACATGGTGCCTTGCGCCTACCA
CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTCACCCTACACTCAAC
CCCCTTATCTACAGTCTGAGGAATCCGAGGTGTGGATGGCTTTGGTCAAAGTGCTTAGCA
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

20

AOLFR78 sequences:

MSPDGNHSSDPTFVLAGLPNLNSARVELFSVFLLVYLLNLTGNVLIVGVVRADTRIQTTPMYF
FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFLGASEFLLAVMSADRYLAICH
PLRYPLLMGAVCFRVALACWVGGLVPVLGPTVAVALLPFCKQGAVVQHFFCDSGPLRLAC
25 TNTKKLEETDFVLASLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI
FLYVRPSQSGSVDTNWAVTVITTFVTPLNPFYIALRNEQVKEALKDMFRKVVAGVLGNLLD
KCLSEKAVK (SEQ ID NO: 145)

30 ATGAGTCCTGATGGGAACACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA
AATCTCAACAGCGCAAGAGTGGAATTATTTTCTGTGTTTCTTCTGTCTATCTCCTGAATCT
GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT
GTACTTCTTTCTGGGTAACCTGTCCCTGCCTAGAGATACTGCTCACTTCTGTCTATTCCTAA
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCTTTGCTGCATGTATCACCCA
ATTCTATTTCTACTTCTTTCTCGGGGCTCCGAGTTCTTACTGTTGGCTGTCATGTCTGCGG
35 ATCGCTACCTGGCCATCTGTATCCTCTGCGCTACCCCTTGCTCATGAGTGGGGCTGTGTG
CTTTCTGTGGCCTTGGCCTGCTGGGTGGGGGACTCGTCCCTGTGCTTGGTCCCACAGTG
GCTGTGGCCTTGCTTCCTTTCTGTAAGCAGGGTGCTGTGGTACAGCACTTCTTCTGCGACA
GTGGCCCACTGCTCCGCCTGGCTTGACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT
CCTGGCCTCCCTCGTCATTGTATCTTCTTGTGATCACTGCTGTGCTACGGCCTCATTG
40 TGCTGGCAGTCTGAGCATCCCTCTGCTTACAGCCGTCAGAAGGCCTTCTCTACCTGTAC
CTCCCACTTGATAGTGGTGACCCTCTTCTATGGAAGTGCCATTTTCTCTATGTGCGGCCAT
CGCAGAGTGGTTCTGTGGACATAACTGGGCACTGACAGTAATAACGACATTTGTGACAC
CACTGTTGAATCCATTCTATGCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA
CATGTTTAGGAAGGTAGTGGCAGGCGTTTTAGGGAATCTTTTACTTGATAAATGTCTCAGT
45 GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

AOLFR79 sequences:

MTPGELALASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMALIFTDSHLQSP
MYFFLNLSFLDICYSSVTPKLLVNFLVSDKSISFEGCVVQLAFFVHVTAESFLLASMA YDR
50 FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANS AIQTGNVFALPFCGPNQLTHYYCDIPLLH
LACANTATARVVLYVFSALVTLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI
FYGTVVFTYVQPHGSTNNTNGQVVSFYTIIIPMLNPFYISLRNKEVKGALQRKLQVNIFFG
(SEQ ID NO: 147)

55 ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCACACCCCACTACCAAGTTCATCT
TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTCTTCGGAGCCATCCTGCTCAT

CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT
 CTCCAAAGCCCAATGTATTTCTTCTCAATGTCCTCTCGTTTCTTGATATTTGTTACTCTTCT
 GTGGTCACACCTAAGCTCTTGGTCAACTTCTGGTCTCTGACAAGTCCATCTCTTTTGAGG
 GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCATGTGACAGCTGAGAGCTTCTGCTGGC
 5 CTCCATGGCCTATGACCGCTTCTTAGCCATCTGTCAACCCCTCCATTATGGTTCTATCATGA
 CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGTCTATGCATTTGGTGGAGCCAACTCCGC
 TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGCCCCAACAGCTAACACACTAC
 TACTGTGACATACCACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG
 TCCTCTATGTCTTTCTGCTCTGGTCAACCTTCTGCCTGCTGCAGTCATTCTCACCTCCTACT
 10 GCTTGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT
 CCACCTGTGCCTCCCACTTTCTGGCCATTGCCATTTTCTATGGCACTGTGGTTTTCACCTAT
 GTTCAGCCCCATGGATCTACTAACAATACCAATGGCCAAGTAGTGTCCGTCTTCTACACCA
 TCATAATTCCCATGCTCAATCCCTTCATCTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC
 TCTGCAGAGGAAGCTTCAGGTCAACATCTTCCCGGCTGA (SEQ ID NO: 148)

15

AOLFR80 sequences:

MEGINKTAKMQFFRPFSPDPEVQMLIFVFLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA
 NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFVFLGGADCVLLVVMAYDRFIAICH
 PLRYRLIMSWSLCVELLVGSVLGFLSLPLTILIFHLPFCHNDEIYHFYCDMPAVMRLACADTR
 20 VHKALYIISFIVLSIPLSLISISYFVIVAILRIRSAEGRQAYSTCSSHLVLLQYGCTSFYLSPS
 SSSPEMGRVVSVAYTFTIPILNPLIYSLRNKELKDALKALRKF (SEQ ID NO: 149)

ATGGAAGGAATAAATAAACTGCAAAGATGCAGTTTTTCTTTCGTCCATTCTCACCTGACC
 CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCTGATGATGTATCTGACCAGCCTCGGTGG
 25 AAATGCTACAATTGCAGTCATTGTTTCAGATCAATCATTCCCTCCACACCCCATGTACTTTT
 TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCATTTGGCCTTG
 GCAAACCTCCTTCAATGGGGCAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT
 TTTTCTTTGCTTCTTGGGTGGGGCTGATTGTGTCTGCTGGTAGTCATGGCTTATGACCGG
 TTTATAGCGATCTGTACCCCTCTGCGATACAGGCTCATCATGAGCTGGTCTTGTGTGTGG
 30 AGCTGCTGGTAGGCTCCTTGGTGTGGGGTCTGTTGTCACTGCCACTCACCATTTTAATC
 TTCCATCTCCCATCTGCCACAATGATGAGATCTACCACTTCTACTGTGACATGCCTGCAGT
 CATGCGCCTGGCTTGTGCAGACACACGCTTCAACAAGACTGCTCTGTATATCATCAGCTTC
 ATCGTCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT
 TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC
 35 TTAGTGGTCTCCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCCCCAGTTCAGCTA
 CTCTCCTGAGATGGGCCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC
 CCCTTGATCTATAGTTTGAGGAACAAGAACTGAAAGATGCCCTAAGGAAAGCATTGAGA
 AAATTCTAG (SEQ ID NO: 150)

40 **AOLFR81 sequences:**

MGVKNHSTVTEFLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIRLNRLHTPMYFFLSS
 LSFLDFCYSSVITPKMMKLWMESHILVETPRSPRMMSNQTLVTEFILQGFSEHPEYRVFLSCF
 LFLYSGALTGNVLTITAFNPLHAPMYFFLLNLATMDICTSSIMPKALASLVSEESSISYGGC
 MAQLYFLTWAASSELLLLTVMAYDRYAAICHPLHYSSMMSKVFCGLATAVWLLCAVNTAIH
 45 TGLMLRLDFCGPNVHHFFCEVPPLLLSCSSTYVNGVMIVLADAFYGIVNFMITIASYGIVSSI
 LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL
 IYTLRNKEVKAALRKLFPFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCCCAGCCCAAGGATG
 50 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT
 ACCGGGTGTTCTTATTCAGCTGTTTCTCTTCTCTACTCTGGGGCCCTCACAGGTAATGTC
 CTCATCACCTTGGCCATCACGTTCAACCCCTGGGCTCCACGCTCCTATGTACTTTTCTTACT
 CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGGCGCTGGCCAGT
 CTGGTGTGCGAAGAGAGCTCCATCTCCTACGGGGGCTGCATGGCCAGCTTATTTCTCA
 55 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTCATGGCCTATGACCGGTACGCAGC
 CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC

ACAGCCGTGTGGCTGCTCTGCGCCGTC AACACGGCCATCCACACGGGGCTGATGCTGCGCT
 TGGATTTCTGTGGCCCCAATGTCATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT
 CTCTCCTGCAGCTCCACCTACGTCAACGGTGT CATGATTGTCCTGGCGGATGCTTTCTACG
 GCATAGTGAACCTCCTGATGACCATCGCGTCCTATGGCTTCATCGTCTCCAGCATCCTGAA
 5 GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCCACCTCACCGTG
 GTGTGCATGTATTACACCGCTGCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG
 CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCCTACCCTCAACCCCT
 CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTCCCTTTCTTC
 AGAAATTAA (SEQ ID NO: 152)

10

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGLLGNLLIISVKASQALKNPMFFFLFYLSL
 SDTCLSTSIAPRMIVDALLKKTTSFSECMIQVFSSHVFGCLEIFILILTAVDRYVDICKPLHYMTII
 SQWVCGVLMVAWVWGSCVHSLVQIFLALSLPFCGPNVINHCFCDLQPLLKQACSETYVVNLLL
 15 VSNSGAICAVSYVMLIFSIVIFLHSLRNHSAEVIKKALSTCVSHIIVILFFGPCIFMYTCPATVFP
 MDKMLIAVFTVGTSLNPNVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT
 GGAAGAAAATAGTGTTTGTATTTTTTTCGCTCTCTACTTGGGAACACTGTTGGGTAAATTT
 20 GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTTCTT
 TTCTACTTATCTTTATCTGATACTTGCCTCTCTACTTCCATAGCCCCTAGAATGATTGTGGA
 TGCCCTTTTGAAGAAGACAACCTATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC
 CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCCTCACGGCTGTTGACCGCTATGTGGA
 CATCTGTAAGCCCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTTTTGATG
 25 GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGCCCTGAGTTT
 GCCATTCTGTGGCCCCAATGTGATCAATCACTGTTTCTGTGACTTGACAGCCCTTGTGAAA
 CAAGCCTGTTCAAGAACCTATGTGGTTAACTACTCCTGGTTTCCAATAGTGGGGCCATTT
 GTGCAGTGAGTTATGTCATGCTAATAATCTCCTATGTCATCTTCTTGCAATTCTCTGAGAAAC
 CACAGTGCTGAAGTGATAAAGAAAGCACTTCCACATGTGTCTCCACATCATTGTGGTCA
 30 TCTTGTCTTTGGACCTTGCATATTTATGTACACATGCCCTGCAACCGTATCCCCATGGAT
 AAGATGTAGCTGTATTTTATACAGTTGGAACATCTTTTCTCAACCCTGTGATTTACACGCT
 GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA
 TGACAAAAGATAA (SEQ ID NO: 154)

35 **AOLFR83 sequences:**

MGNWTAAVTEFVLLGFSLSREVELLLLVL LPTFLLTLLGNLLIISTVLSCSR LHTPMYFFLCNL
 SILDILFTSVISPKVLANLGS RDKTISFAGCITQCYFYFFLGTVEFLLLTVM SYDRYATICPLRYT
 TIMRPSVCIGTVVFSWVGFLSVLP TILISQLPFCGSNIINHFFCDSGPLLALACADTTAIELMDF
 MLSSMVLCCIVLVAYSITYIILTIVRIP SASGRKKAFNTCASHLTIVIPSGITVFIYVTPSQKEYL
 40 EINKIPLVLSSVVTPLNPFITL RNDTVQGVLRDVWVRVRGVFEKRMRAVLRSRLSSNKDHQ
 GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

ATGGGTAAGTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG
 AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCACGTTCCCTGCTGACTCTTCTGGGGAA
 45 CCTGCTCATCATCTCCACTGTGCTGCTCCTGCTCCCGCCTCCACACCCCCATGTA CTCTTCT
 TGTGCAACCTCTCTATCCTGGACATCCTCTTCACTCAGTCATCTCTCCAAAAGTGTGGCC
 AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTCTT
 ACTTTTTCTTGGGCACAGTTGAGTTCTCTCTGCTGACGGTCATGTCTATGACCGTTATGCC
 ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCATTGGGACCG
 50 TTGTATTCTCTTGGGTGGGAGGCTTCCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCAG
 CTGCCCTTCTGTGGCTCCAATATCATTAACCACTTCTTCTGTGACAGTGACCCCTTGCTGGC
 CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC
 ATCCTCTGCTGCATAGTCCTCGTGGCCTATTCTATACGTACATCATCTTGACCATAGTGCG
 CATTCTTCTGCAAGTGGAAGGAAGAAGGCCTTTAATACCTGTGCTTCCACCTGACCATA
 55 GTCATCATTCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCAGAAAGAATATCT
 GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGACTCCATTCTCAACCCCTTT

ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCCTCAGGGATGTGTGGGTCAGGGTT
CGAGGAGTTTTTGAAGAGGATGAGGGCAGTGTGAGAAGCAGATTATCCTCCAACAAA
GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGT
AG (SEQ ID NO: 156)

5

AOLFR85 sequences:

MGAKNNVTEFVLFGFLFESREMQHTCFVVFFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLTQVLPFCGPNEIDNFFCDVHPLLKLACADTYMV
GLIVVANSGLMISLASFILIIISYVILLNLRSQSSDDRKA VSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLIILFNIVMPPLLNPLIYTLRNNVDKNAMEKRLFRVKRSLGEK (SEQ ID NO: 157)

10

ATGGGTGCCAAGAACAATGTGACTGAGTTTGTGTTTATTTGGCCTTTTTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCCTCTTTCATGTGCTCACTGTCCTGGGGAACCTT
CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCTCTGA
GCCAGTTGTCTTTTGTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC
ACTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCA
CTTCTTTGGTGGCACTGAGATCTTCCTCCCTTACAGCCATGGCCTATGACCGCTATGTGGCC
ATCTGTAGGCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
GGGCCTCCTGGTTAGCTGGCTTCCTGCATTCCATCCTGCAGACCCTCCTCACGGTTCAGCTG
CCTTTTGTGGGCCCAATGAGATAGACAACCTTCTTCTGTGATGTTTCATCCCCTGCTCAAGTT
GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT
TTAGCATCCTTTTATCCTTATCATTTCTATGTTATCATCTTACTGAACCTAAGAAGCCA
GTCATCTGAGGACCGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCTT
TTGGTTCTCATGCCCCCATGTTTCATGTACATTTCCTCCCTCCACCACCCTGGCTGCTGACAA
ACTTATCATCCTCTTTAACATTGTGATGCCACCTTTGCTGAACCCTTTGATCTATACACTAA
GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG
AGAAGTGA (SEQ ID NO: 158)

20

25

AOLFR86 sequences:

MQVLVLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVFFLLIYVVTVC
GNMLIVVITITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF
LGGVBIILLTVMAYDRYVAICKPLHNTTMRHLICAMLVGVAVLGGFLHSLVQLLLVLWLPFC
GPNVINHFACDLYPLLEVACTNTYVIGLLVANSGLICLLNFLMLAASYTVILYSLRSHSADGRC
KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR
KLFTW (SEQ ID NO: 159)

35

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
CTCAGTGACCTTGAATCTATGGACATAACCACAAAATATCACAGAATTTTTTCATGCTGGGG
CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTGTGATCTATGTGG
TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC
CCCTGTGTATTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC
TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG
GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
CTTATGACCGCTATGTGGCCATCTGTAAGCCCCTGCACAATACTACCATCATGACCAGGCA
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCCTGCATTCAATTGGTTTCA
CTCCTCCTGGTCCTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTTGCCTGTGA
CTTGTAACCTTTGCTGGAAGTTGCCTGCACCAATACGTATGTCATTGGTCTGCTGGTGGTT
GCCAACAGTGGTTAATCTGCCTGTTGAACCTCCTCATGCTGGCTGCCTCCTACATTGTCAT
CCTGTACTCCTTGAGGTCCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
GCCCACTTCATTGTTGTTGCCTTGTCTTTGTGCCCTGTATTTTACTTATGTGCATCCATTT
TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA
TCCACTCATTTATACCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACA
TGGTAA (SEQ ID NO: 160)

55

AOLFR87 sequences:

MNNAIQLSLGFIDLGPSVLQKILLTKILLFKMYVSNCPNCAIHRKINYPNTKLDSEQVNNITEFI
 LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIVVTTTTSPALDSPVYFFLSFFSFIDGCSSTMAP
 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVAICKPLYLITMNRQVCGL
 5 LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLLKLSCTDTHVFLGFAANSGLM
 CMLIFSILITSYVLILCSQRKALSTCAFHITVVVLFVPCILVYLRPMITFPIDKAVSVFYTVVTPM
 LNPLIYTLRNTEVKNAMKQLWSQIHWGNLDCD (SEQ ID NO: 161)

ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC
 10 AGAAAATAATCCTGACCAAAATTATTTTATTGTTCAAATGTATGTGTCAAATTGCAATCC
 TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAACTGGATTTCGAGCAAGTGAAC
 AACATAACGGAATTCATCTTGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT
 TTGCTGTGTTTACACTCATCTACTTTCTCACCATGGTAGACAACCTAATCATTGTGGTGACA
 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGATTTTTTCTGTCTTTCTTTCTCTTCAT
 15 AGATGGCTGCTCCTCTTCTACCATGGCCCCAAAATGATATTTGACTTACTCACTGAAAAG
 AAAACTATTTCTTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG
 TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCCT
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTG
 GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTTCTGTGGCCC
 20 CAATGTCAATTGACCATTTCATCTGTGACCTTTCCCTCTGCTAAACTCTCCTGCACTGACA
 CTCACGTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT
 ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTACCTGCGC
 CTTCCATATCACTGTAGTCGTCCTATCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA
 TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTATACTGTGGTAACACCCATGTTA
 25 AACCCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

MWQKNQTSLADFILEGLFDDSLTHLFLSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
 30 LSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYLCLGGAEFCFLAVMSYDRYVAICH
 PLRYAVLMNKKVGLMMAVMSWLGA SVNSLIHMAILMHFPFCGPRKVYHFYCEPPAVVKLVC
 GDITVYETTVYISSILLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVS LWFACIFS
 YMRPRSQCTLLQNKVGSVFYSITPTLNSLIYTLRNKDVAKALRRVLRDVTQCIQRLQLWLP
 RV (SEQ ID NO: 163)

ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT
 CCCTTACCCACCTTTTCTTTTCTCCTTGACCATGGTGGTCTTCTTATTGCGGTGAGTGGC
 AACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCT
 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT
 40 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC
 TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCATGTCCTATGACCGCTAT
 GTTGCCATCTGTATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA
 TGGCTGTATGTCATGGTTGGGGGCATCCGTGAACTCCCTAATTCACATGGCGATCTTGAT
 GCACTTCCCTTTCTGTGGGCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCAGCTGTTG
 45 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGATACATCAGCAGCATTCT
 CCTCCTCCTCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCAATTCA
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCCTTGCCACTTGTTGGCTCCACCTCACGGTG
 GTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGGTCCAGTGCATCT
 ATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCACATTGAATTCTCTG
 50 ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT
 GTTATCACCCAGTGCAATTCAACGACTGCAATTGTGGTTGCCCCGAGTGATAG (SEQ ID NO:
 164)

AOLFR89 sequences:

MLDPSISSHTLYLHSLFPQGLRKGTMWQKNQTSLADFILEGLFDDSLTHLFLSLTMVVFLIAVS
 55 GNTLTILLICIDPQLHTPMYFLLSQSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYL

CLGGAECFLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWL GASVNSLIHMAILMHF
PFCGPRKVYHFYCEFPVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSK
RNAFATCGSHLTVVSLWFGACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
KALRRVLRRDVITQCIQRLQLWLPRV (SEQ ID NO: 165)

5

ATGCTGGACCCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT
GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG
GCTCTTCGATGACTCCCTTACCCACCTTTTCTCTTCTCCTTGACCATGGTGGTCTTCCTTAT
TGCGGTGAGTGGCAACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA
10 CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
ACCCAGCACTTCCTCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCTATGTC
CTATGACCGCTATGTTGCCATCTGTCTCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAG
GTGGGACTGATGATGGCTGTCTATGTCATGGTTGGGGGCATCCGTGAACCTCCCTAATTGACA
15 TGGCGATCTTGATGCACTTCCCTTTCTGTGGCCTCGGAAAGTCTACCACTTCTACTGTGA
GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
ATCAGCAGCATTCTCCTCCTCCTCCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTT
CAAAGTGTCTTATGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT
CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG
20 TCCCAGTGCACCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA
CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCGGAGTG
TAG (SEQ ID NO: 166)

25 AOLFR90 sequences:

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPVQEI VVFLVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLHSMIQLFTFQLPFCGPNVINHFMC DLYP LLELACTDTHIFGLMVVINS
30 FICINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPSPAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRMLMVVSDEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACTTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAAATTTCTTTGTCCTAATTGCAGACTATA
35 CATGATCCCTGTTGGAGCTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTGCGGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTG
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATCTC
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTGGA
TGCGTGCTTCTCATCTGTCTACCCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
40 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
GGCCTCTTGCAATCCATGATACAAATCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
45 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
50 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

MGNWSTVTEITLIAFPALLEIRISLFVVLVVTYTLTATGNITHISLIWIDHRLQTPMYFFLSNLSFL
55 DILYTTVTIPKLLACLLGEEKTISFAGCMIQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI
MNSRACLLLVLCWVGAFSLSVLFPTIVVTRLPHYCRKEINHFFCDIAPLLQVACINTHLIEKINFL

SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD
YDKVA AVLITVVTPLNPFYISLRNEKVQEVLRVETVNRIMTLIQRKT (SEQ ID NO: 169)

ATGGGAAACTGGAGCACTGTGACTGAAATCACCCCTAATTGCCTTCCCAGCTCTCCTGGAGA
5 TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAAACAGCAACAGGAAACAT
CACCATCATCTCCCTGATATGGATTGATCATCGCCTGCAAACCTCCAATGTACTTCTTCTCTCA
GTAATTTGTCCCTTTCTGGATATCTTATACACCACTGTGATTACCCCAAAGTTGTTGGCCTGC
CTCCTAGGAGAAGAGAAAACCATATCTTTTGTGCTGGTTGCATGATCCAAACATAATTTCTACT
TCTTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCCTTTGACCGCTACATGGC
10 TATCTGCGACCCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT
CTGGGATGCTGGGTGGGAGCCTTCTGTCTGTGTTGTTTCCAACCATTGTAGTGACAAGGC
TACCTTACTGTAGGAAAGAAATTAATCATTTTCTTCTGTGACATTGCCCCCTCTTCTCAGGTG
GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTATCCT
GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAATTTCTACCCTCTGCGTATCC
15 CCTCCACCCAGGGCCGTCAGAAAGCTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC
ATTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT
ATGACAAGGTGGCCGCTGTCCTCATCAGTGGTGACCCCTCTCCTGAACCCCTTTTATCTA
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGAGACAGTGAACAGAATCATGAC
CTTGATACAAAGGAAAACCTGA (SEQ ID NO: 170)

20

AOLFR92 sequences:

MRNGTVITEFILLGFPVIQGLQTPLFIAIFLTYYLTLAGNGLIATVWAEPRLOIPMYFFLCNLSFLE
IWYTTTIVPKLLGTFVVARVICMSCLLQAFFHFFVGTTEFLITIMSFDRLYTICNPLHPTIM
TSKLCLQLALSSWVVGFTIVFCQTMLLIQLPFCGNNVISHFYCDVGPSLKAACIDTSILELLGVIA
25 TILVIPGSLLFNMISYIYLSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
INKVSVLNTILTPLNPFYITIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC
TACAAACACCTCTCTTTATTGCAATCTTCTCACCTACATATTAACCCTTGCAGGCAATGGG
30 CTATTATTGCCACTGTGTGGGCTGAGCCAGGCTACAAATTCCAATGTACTTCTTCTCTTG
TAACTTGTCTTTCTTAGAAATCTGGTACACCACCACAGTCATCCCCAACTGCTAGGAACC
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCCTGCTGCAGGCCCTTCTCCACT
TCTTCGTGGGCACCACCGAGTTCTTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC
ATCTGCAATCCCCCTTCAACACCCCAACATCATGACCAGCAAACCTCTGCCTGCAGCTGGCCC
35 TGAGCTCCTGGGTGGTGGGCTTACCATTGTCTTTTGTGACAGATGCTGCTCATCCAGTT
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCCCAGTTTGAAA
GCCGCTGCATAGACACCAGCATTTTGAACCTCCTGGGCGTCATAGCAACCATCCTTGTGA
TCCCAGGGTCACTTCTCTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA
ATTCTTTCAGCCACTGGCCACCAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT
40 CTCCTGCTCTACGGGGCTGTTCTGTTTCATGTACCTAAGACCCACAGCACACTCCTCCTTAA
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCCCTTCTGAATCCCTTTATT
TATACTATTAGAAACAAGGAGGTGAAGGCGCTTAAGAAAGGCAATGACTTGCCCAAAG
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

45 **AOLFR93 sequences:**

MLMNYSSATEFYLLGFPSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHL
SALEILVTTHVPVMLWGLLLPGMQTYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
PLRYNIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTYCKSNVNNFFCDRGQLKLSCN
NTLFTEFILFLMAVFVLFGLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY
50 VKPKQTQAADYNWVVSMLMVSVVTPLNPFIFITLRNDKVIEALRDGVKRCCQLFRN (SEQ ID
NO: 173)

ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA
ACTACATCATATCCTTTTGTATATTCTTCTTTTCTACTTGGTGACATTAATGGGAAACA
55 CAGTCATCATGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCTCT
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCCGTGATGCTTTGGG

GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG
 TACCTTGCTGTGGGGACAACAGAGTTTCGATTACTTGGAGCAATGGCTGTGGACCGTTATG
 TGCTGTCTGTAAACCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT
 GGTCTTGTGTCATGGGTGTTTGGGTTTCTTTTTCAAATCTGGCCGGTCTATGTCATGTTTC
 5 AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGCAATTGCT
 CAAACTATCCTGCAATAATACTCTTTTCACGGAGTTTATCCTCTTCTAATGGCTGTTTTTG
 TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATTCTC
 AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG
 TGTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACGCAGGCA
 10 GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACTCCTTCTCAATCCTTT
 CATCTTCACCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
 TGTCAACTATTCAGGAATTAG (SEQ ID NO: 174)

AOLFR94 sequences:

15 METWVNQSYTDGFFLLGIFSHSTADLVLFVSVMAVFTVALCGNVLLIFLIYMDPHLHTPMYFF
 LSQLSLMDLMLVCTNVPKMAANFLSGRSISFVCGIQLFVCLVGSEGLLLGLMAYDRYVA
 ISHPLHYPLMNQVRVCLQITGSSWAFGIIDGLIQMVVMNFPYCGLRKVNHFCEMLSLLKLAC
 VDTSLFEKVIFACCVFMLLPFSIIVASYAHILGTVLQMHSAQAWKKALATCSSHLTAVTLFYG
 AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
 20 (SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAAGTCCTACACAGATGGCTTCTTCTCTTAGGCATCTTCTCCC
 ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT
 GGAATGTCCTCCTCATCTTCTCATCTACATGGACCCTCACCTTCACACCCCCATGTACTT
 25 CTTCCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG
 GCAGCCAACTTCTCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATACAAATTG
 GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGTCTGGGACTCATGGCTTATGACCG
 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC
 AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
 30 AATGAATTTCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCT
 TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGTCTGTG
 TCTTCATGCTTCTTCTCCATTCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT
 GTGCTGCAAATGCACTCTGCTCAGGCCTGAAAAAGGCCCTGGCCACCTGCTCCTCCCACC
 TGACAGCTGTCACCCTCTTCTATGGGGCAGCCATGTTTCATCTACCTGAGGCCTAGGCACTA
 35 CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCCTTACTCCCATGCTC
 AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG
 GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

AOLFR95 sequences:

40 MLGSKPRVHLYILPCASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL
 GNVGMMTIIMTDPRLNTPMYFFLGNLSFIDLFYSSVIEPKAMINFWSENKISIFAGCVAQLFLFA
 LLIVTEGFLLAAMAYDRFIAICNPLLYSVQMSTRCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS
 RAVDHFYCDRPLQRLSCSDLFIHRMISFSLSCHILPTHIVIVSYMYTVSTVLKIHSTEGHKKAFST
 CSSHLGVVSVLYGAVFFMYLTPDRFELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE
 45 KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC
 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGCAGG
 CTTACAGGGTACGCCAGAGCTCCACATTCTCCTCTTCTGCTATTTTTGTTTGTATGCCA
 50 TGATCCTTCTAGGGAATGTTGGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC
 ACCAATGTATTTTTCTAGGCAATCTCTCCTTCATTGATCTTTTCTATTCTGTTATTGA
 ACCCAAGGCTATGATCAACTTCTGGTCTGAAAACAAGTCTATCTCCTTTGCAGGCTGTGTG
 GCCCAGCTCTTTCTTTTCCCTCCTCATTGTGACTGAGGGATTTCTCCTGGCGGCCATGGC
 TTATGACCGCTTTATTGCCATCTGCAACCTCTGCTCTACTCTGTTCAAATGTCCACACGTC
 55 TGTGTACTCAGTTGGTGGCTGGTTCTATTTTGTGGCTGCATTAGCTCAGTTATTGAGACT
 AGCATGACATTTACTTTATCTTTTTGCGCTTCTCGGGCTGTTGACCACTTTACTGTGATTC

TCGCCCCACTTCAGAGACTGTCTTGTTCTGATCTCTTTATCCATAGAATGATATCTTTTTCTCT
TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG
TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTTTTTATGTATCTCACTCCTGAC
5 AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA
ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAATTTCTAGA
GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

AOLFR96 sequences:

10 MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAIYTVTLGNFLIVTVTSVDLALQTPMYFFLQN
LSLLEVCFTLVMPKMLVDLVSPRKIIISFVCGQTQMYFFFFGSSECFLSMAYDRFVAICNP
LHYSVIMNRSCLWMAIGSWMSGVPVSMQLTAWMMALPFCGPNVDFHFFCDGPPVLKLVTV
DTTMYEMQALASTLLFIMFPFCLILVSYTRIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL
TYLRPKSNQSPESKKLVLSYTVITPMLNPIIYGLRNNEVKGAVKRTITQKVLQKLDVF (SEQ
15 ID NO: 179)

ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC
CCGAGATGCAAGTTTCCCTCTTTATTTTTTCTTGGCCATTTATACAGTCACTTTGTTGGGC
AACTTTCTTATTGTACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT
20 TCTTCAAAATCTGTCACTTCTTGAAGTATGTTTCACCTTGGTTATGGTGCCAAAAATGCTTG
TAGATCTAGTGTCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT
CTTCTTCTTCTTGGCAGTTCTGAATGTTTCTTCTCTCCATGATGGCTTATGATCGCTTGTG
GGCCATCTGTAACCCCTCTCCATTATTACAGTCATAATGAACAGGTCCCTATGCTTGTGGATG
GCCATAGGCTCTTGGATGTCCGGTGTCTCTGTGTCTATGCTACAGACAGCTTGGATGATGG
25 CCCTTCTTCTGTGGACCAAATGCCGTGGACCACTTTTTCTGTGATGGTCCCCCAGTGTTA
AACTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTTGCTCCACACTCCTGT
TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGCATTATCATAACAATTCTG
AGGATGTCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT
GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCCAAATCAAACAGTCC
30 CCTGAGAGCAAGAAGCTAGTGTCTTGTCTTACTGTCTCATCACACCTATGCTAAACCCCA
TCATCTACGGCCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAA
AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

AOLFR97 sequences:

35 MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMVVPFSIAEHWRMRMKGANLSQGMFEL
LGLTTDPQLQRLFLVFLGMYTATLLGNLVMFLHLHVSATLHTPMYSLKLSLDFCYSSSTVV
PQTLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLLAAMAYDRYAAICNPILYSTIMSPEVC
ASLIVGSYSAGFLNSLIHTGCFSLKFCGAHVVTHFFCDGPPILSLSCVDTSLEILLFIFAGFNLLS
CTLTILISYFLILNTILKMSSAQGRFKAFTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRTVA
40 VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
CCTTAGGCAGAATTAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT
45 GGAGTTTGAGCTCTTGGGCCTCACCCTGACCCCGAGCTCCAGAGGCTGCTCTTCGTGGTG
TTCCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTTCATGTTCTCCTGATCCATG
TGAGTGCCACCCCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCCTTCTTGGATTTC
TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGGTGAACCTCTTGGCCAAGAGGAAAGTGA
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACAGTGAAGTGC
50 TATCTCATCGCTGCCATGGCCTATGACCGCTATGCCGCTATTTGTAACCCCTGCTCTACTC
AACCATCATGTCTCCTGAGGTCTGTGCCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC
CTCAATTCTCTTATCCACACTGGCTGTATCTTTAGTCTGAAATTCTGCGGTGCTCATGTCTG
CACTCACTTCTTCTGTGATGGGCCACCCATCCTGTCTTGTCTTGTGTAGACACCTCACTGT
GTGAGATCCTGCTCTTCATTTTGTCTGGTTTCAACCTTTTGAGCTGCACCCTACCATCTTG
55 ATCTCCTACTTCTTAATTCTCAACACCATCCTGAAAATGAGCTCGGCCAGGGCAGGTTTA
AGGCATTTTCCACCTGTGCATCCACCTCACTGCCATCTGCCTCTTCTTGGCACAACTT

TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA
TCTACACAGTGGTGATCCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

5 **AOLFR98 sequences:**

MRGFNKTTVVVTQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLEI
LSFSESCYTFVIIPQLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLIAVMGYDRYVAICHPLR
YTLINKRLGLELISLGSATGFFIALVATNLCDMRFCGPNRVNHYFCDMAPVKLACTDTHVKE
LALFSLSILVIMVPFLLILISYGFIVNTILKIPSAEGKKAFTVCASHLTVVVFVHYGCASIYLRPKSK
10 SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC
TGGGGGAGCTCCAGCTGCTGCTTTTGTGCATCTTTCTTCTCCTATACTTGACAATCCTGGTG
GCCAATGTGACCATCATGGCCGTATTTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG
15 GCTTTCATTCATCCTTTTCAATTTCTGAGTCCTGCTACACTTTTGTGCATCATCCCTCAGCTGC
TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT
CTTTTCTCCTGGCTTTGCTTGCACCAACTGCCCTCCTCATTGCTGTGATGGGATATGATCGCT
ATGTAGCAATTTGTACCCCTCTGAGGTACACACTCATATAACAAAAGGCTGGGGTTGGA
GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATTT
20 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCCTATTTCTGTGACATGGCACCTGT
TATCAAGTTAGCCTGCATGACACCCCATGTGAAAGAGCTGGCTTTATTAGCCTCAGCATC
CTGGTAATTATGGTGCCTTTTCTGTTAATTCTCATATCCTATGGCTTCATAGTTAACACCAT
CCTGAAGATCCCTCAGCTGAGGGCAAGAAGGCCTTTGTACCTGTGCCTCACATCTCACT
GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC
25 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT
CTTGCTACAGTCTGAGGAACAAAGAGGTAAAACTGCATTGAAAAGAGTTCTTGGAATG
CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

AOLFR99 sequences:

30 MERVNETVVREVIPLGFSSRLARLQQLLFVIFLLLYLFTLTGNAMISTIVLDRALHIPMYFFLAILSC
SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV
LMGHGVCMGLVAAACACGFTVAQIITSLVFHLPFYSSNQLHHFFCDIAPVLKLASHHNFHSQIV
IFMLCTLVLAIPLLLILVSYVHLSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFIYLRPQSNY
SSSQDALISVSYTHITPLFNPMIYSLRNKEFKSALCKIVRRITISLL (SEQ ID NO: 185)

35 ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC
AATGCAATCATCATTTCCACCATTGCTCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT
CCTTGCCATCCTCTCTTGCTCTGAGATTGCTACACCTTCATCATTTGTACCCCAAGATGCTGG
40 TTGACCTGCTGTCCCAGAAGAAGACCATTTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
TTCTCTTCTTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA
GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTCA
CCTGCCTTTTTATTCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGTCTCA
45 AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC
CTGGCTATCCCTTATTGTTGATCTTGGTGTCTATGTTACATCCTCTCTGCCATACTTCA
GTTTCTTCCCACTGGGTAGGTGCAAAGCTTTTTCTACCTGTGTATCTCACCTCATTATTG
TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAACTACTCCTCA
AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA
50 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAAATTGTGAGAAGAACAAT
TTCCCTGTTGTAA (SEQ ID NO: 186)

AOLFR101 sequences:

55 MDTGNWSQVAEFILGFPHLQGVQIYFLLLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI
LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
HYPTLMTPTLCABIAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDFPPVLSLACTDTSINV

LVDFVINSCKILATFLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVLFYGSILSMYVQLK
KSYSLDYDQALAVVYSVLTPLNPFIFYSLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

5 ATGGACACAGGGAAGTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCATCTCC
AGGGTGTCCAGATTTATCTCTTCTCTTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA
AACCTGCTGATATTCCTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT
TTGTCAGCATTCCTCTCTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG
GCAAACCTTGCTCAGTGAGAAAAAGACCATTTCATTCTCTGGGTGTCTCCTGCAGATCTATT
TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA
10 TTTAGCCATCTGCCGCCCCCTCCACTACCCAACCCTCATGACCCCAACACTTTGTGCAGAG
ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTCCTTGATT
CACGCCTCCCATTCGTGGCCCCAATCGCATTACAGCACGTCTTTTGTGACTTCCCTCCTGTG
CTGAGTTTGGCTTGCACTGATACGTCTATAAATGTCCTAGTAGATTTTGTATAAATTCCTG
CAAGATCCTAGCCACCTTCTGCTGATCCTCTGCTCCTATGTGCAGATCATCTGCACAGTGC
15 TCAGAATTCCTCAGCTGCCGGCAAGAGGAAGGCCATCTCCACGTGTGCCTCCCACTTCAC
TGTGGTTCTCATCTTCTATGGGAGCATCCTTTCCATGTATGTGCAGCTGAAGAAGAGCTAC
TCACTGGACTATGACCAGGCCCTGGCAGTGGTCTACTCAGTGCTCACACCCCTCCTCAACC
CCTTCATCTACAGCTTGCGCAACAAGGAGATCAAGGAGGCTGTGAGGAGGCAGCTAAAGA
GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

20

AOLFR102 sequences:

MPVGKLVFNQSEPTFVFRAFTTATEFQVLLFLLFLLLYLMILCGNTAIWVVCVTHSLRTPMYF
FLSNLSFLELCYTTVVVPLMLSNILGAQKPISLAGCGAQMFFVTLGSTDCFLLAIMAYDRYVAI
CHPLHYTLIMTRELCTQMLGGALGLALFPSLQLTALIFTLPFCGHHQEIHFCDVPPVRLACA
25 DIRVHQAFLYVVSILVLTPIFLICVSYVFITCAILSIRSAEGRRRAPSTCSFHLTVVLLQYGCCSL
VYLRPRSSTSEDEDSQIALVYTFVTPLNPLLYSLRNKDKVKGALRSAIRKAASDAN (SEQ ID
NO: 189)

30 ATGCCTGTGGGGAACTTGTCTTCAACCAGTCTGAGCCCACTGAGTTTGTGTTCCGTGCGT
TCACCACAGCCACTGAATTCAGGTTCTTCTCTTCTCTCTCCTCCTCCTCTACTTGATG
ATCCTCTGTGGCAACACAGCCATCATCTGGGTGGTGTGCACACACAGCACCCCTCCGCACCC
CGATGTATTTCTTCTGTCCAACCTGTCTTTCTTGGAACTCTGCTACACCACCGTGGTAGTA
CCCTTGATGCTTTCCAACATTTTGGGGGGCCAGAAGCCCATTTCTGTTGGCTGGATGTGGGG
CCCAAATGTTCTTCTTGTACCCCTCGGCAGCACGGACTGTTTCTCTTGGCGATCATGGCC
35 TATGACCGCTATGTGGCTATCTGCCACCCGCTGCACTACACCCTCATCATGACCCGCGAGC
TGTGCACGCAGATGCTGGGTGGGGCCCTGGGCCTGGCCCTCTTCCCTCCTGCACTCAC
CGCCTTAATCTTCAACCCTGCCCTTTTGGCGCCACCACCAGGAAATCAACCACTTCTCTGCG
ATGTGCTTCCCGTCTGCGCTGGCCTGCGCTGACATCCGCGTGCACACAGGCTGTCTCTA
TGTCGTGAGCATCCTCGTGCTGACCATCCCTTCTGCTCATCTGCGTCTCCTACGTGTTCA
40 TCACCTGTGCCATCCTGAGCATCCGTTCTGCCGAGGGCCGCCGCCGGGCTTCTCCACCTG
CTCCTTCCACCTCACCGTGGTCTGCTGCAGTATGGCTGCTGCAGCCTCGTGTACCTGCGTC
CTCGGTCCAGCACCTCAGAGGATGAGGACAGCCAAATCGCGTTGGTCTACACCTTTGTAC
CCCCTTACTCAACCTTTGCTTTACAGCCTTAGGAACAAGGATGTCAAAGGTGCTCTGAGG
AGTGCCATTATCCGTAAAGCAGCCTCTGACGCCAACTGA (SEQ ID NO: 190)

45

AOLFR103 sequences:

MAEMNLTLVTEFLIAFTEYPEWALPLFLLLFMYLITVLGNLEMILILMDHQLHAPMYFLLSH
LAFMDVCYSSITVPQMLAVLLEHGAALSRYTRCAAQFFLTFGSDICYLLALMAYDRYLAVCQ
PLLYVTILTQARLSLVAGAYVAGLISALVRTVSAFTLSFCGTSEIDFIFCDLPPLLKLTGSESYT
50 QEVLIMFAIFVIPASMVVILVSYLFIIAIMGIPAGSQAKTFSTCTSHLTA VSLFFGLTIFMYLRG
NSDQSSEKNRVVSVLYTEVIPMLNPLYSLRNKEVKEALRKILNRAKLS (SEQ ID NO: 191)

55 ATGGCAGAGATGAACCTCACCTTGGTGACCGAGTTCCTCCTTATTGCATTCACTGAATATC
CTGAATGGGCACTCCCTCTCTTCTCTTGTATTATTATGTATCTCATACCGTATTGGGG
AACTTAGAGATGATTATTCTGATCCTCATGGATCACCAGCTCCACGCTCCAATGTATTTCCT
TCTGAGTCACCTCGCTTCATGGACGTCTGCTACTCATCTATCACTGTCCCCAGATGCTGG

CAGTGTCTGCTGGAGCATGGGGCAGCTTTATCTTACACACGCTGTGCTGCTCAGTTCTTTCT
 GTTACCTTCTTTGGTTCCATCGACTGCTACCTCTTGGCCCTCATGGCCTATGACCGCTACT
 TGGCTGTGTGCCAGCCCCTGCTTTATGTACCATCCTGACACAGCAGGCCCGCTTGAGTCT
 TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGTGCCTTGGTGCGGACAGTCTCAGCCTTC
 5 ACTCTCTCCTTCTGTGGAACCAGTGAGATTGACTTTATTTTCTGTGACCTCCCTCCTCTGTT
 AAAGTTGACCTGTGGGGAGAGCTACACTCAAGAAGTGCTGATTATTATGTTTGCCATTTTT
 GTCATCCCTGCTTCCATGGTGGTGATCTTGGTGTCTACCTGTTTATCATCGTGGCCATCAT
 GGGGATCCCTGCTGGAAGCCAGGCCAAGACCTTCTCCACCTGCACCTCCCACCTCACTGCT
 GTGTCACTCTTCTTTGGTACCCTCATCTTCATGTACTTGAGAGGTAACCTCAGATCAGTCTTC
 10 GGAGAAGAATCGGGTAGTGTCTGTGCTTTACACAGAGGTATCCCCATGTTGAATCCCCCTC
 ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCTCAATAGAGCC
 AAGTTGTCCTAA (SEQ ID NO: 192)

AOLFR105 sequences:

15 MQGLNHTSVSEFILVGFSAPHLQLMLFLLFLLMYLFTLLGNLLIMATVWSERSLHMPMYLFLC
 ALSITEILYTVANPRMLADLLSTQRSIAFLACASQMFSSFSFGFTHSFLLTVMGYDRYVAICHPL
 RYNVLSLRGCTCRVGCWSWAGGLVMGMVVTSAlFHLAFCGHKEIHFFCHVPPLKLACGDD
 VLVVAKGVLVCITALLGCFLLILLSYAFIVAAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS
 VTYLKPKGPQSPEGDTLMGITYTVLTPFLSPIIFSLRNKELKVAMKKTCFTKLFPQNC (SEQ ID
 20 NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCCTTCCC
 CCACCTCCAGCTGATGCTCTTCTGCTGTTCTGCTGATGTACCTGTTACGCTGCTGGGCA
 ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT
 25 CCTGTGTGCCCTCTCCATCACCGAGATCCTCTACACCGTGGCCATCATCCCCGCGCATGCTG
 GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCTGCGCTGTGCCAGTCAGATGTTCTT
 CTCCTTCAGCTTCGGCTTCACCCACTCCTTCTGCTCACTGTCTGCGGCTACGACCGCTACG
 TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
 GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCACTGGGGATGGTGGTGACCTCGGCCATTTTC
 30 CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTTCTTCTGCCACGTGCCACCTCTGTT
 GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT
 CACGGCCCTGCTGGGCTGTTTTCTCCTCATCCTCCTCTCCTATGCCTTCATCGTGGCCGCCA
 TCTTGAAGATCCCTTCTGCTGAAGGTGCGGAACAAGGCCTTCTCCACCTGTGCCTCTCACCT
 CACTGTGGTGGTGTGCTGCACTATGGCTTTGCTCCGTCAATTAACCTGAAGCCCAAAGGTCCC
 35 CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCTCACACCTTCTCTCA
 GCCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTGCGCATGAAGAAGACTTGCTT
 CACCAAACCTTTCCACAGAAGTCTGA (SEQ ID NO: 194)

AOLFR106 sequences:

40 METANYTKVTEFVLTGLSQTPEVQLVLFVIFLSFYLFILPGNLIICTISLDPHLTSPMYFLLANLA
 FLDIWYSSITAPEMLIDFFVERKIIISFDGCIQLFFLHFAGASEMFLLTVMAFDLYTAICRPLHYA
 TIMNQRLCCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRACANTFPEELVM
 ICSSGLISVVCLIALLLMSYAFLLALFKLSGSGENTNRAMSTCYSHITIVLMFGPSIYIYARPD
 SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

45 ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
 CAGAGGTCCAAGTCTATTTGTTATATTTCTATCCTTCTATTTGTTATCTTACCAGGA
 AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTTCTT
 GTTGGCTAATCTGGCCTTCTTGTATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA
 50 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGTGATGGATGCATTGCACAGCTCTTCTT
 CTTACACTTGTGTTGGGCTTCGGAGATGTTCTTGTCTCACAGTGATGGCCTTTGACCTCTACA
 CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG
 GTGGCTCTCTCTGGAGGGGGGGCTTCATTCTATCATACAGGTGGCTCTCATTGTTT
 GACTTCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTGT
 55 CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG
 ATCTCTGTGGTGTGTTGATTGCTGTGTAATGTCTATGCCTTCTTCTGGCCTTGTTCAT

GAAACTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACATT
 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCGTT
 TTCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCCTTTACGTAATCCCATT
 TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAAAATATA
 5 TTTTGTGTAAAGAGAAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

MELWNFTLGSGFILVGILNDSGSPELLCATITILYLLALISNGLLLLAITMEARLHMPMYLLGQ
 LSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFLALTMGGAEDLLAFMAYDRYVAICH
 10 PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYPCRAQEIRHLLCEIPHLLKVACAD
 TSTRYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPSNEGRKKALVTCSSHLTUVGMFYGA
 ATFMVYLPSSFHSTRQDNISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKYMLPAHSTL
 (SEQ ID NO: 197)

15 ATGGAGCTCTGGAACCTTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG
 CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCCGGCTCCACATGCCCATGTACCTC
 CTGCTTGGGCAGCTCTCTCATGGACCTCCTGTTACATCTGTTGTCACTCCCAAGGCCCT
 TGCGGACTTTCTGCGCAGAGAAAAACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTT
 20 CTGGCACTGACAATGGGTGGTGTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT
 ATGTGGCCATTTGTATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT
 CATGGTGGCCACGTCTGGATCCTGGCATCCCTAAGTGCCCTAATATATACCGTGTATACC
 ATGCACTATCCCTTCTGCAGGGCCCAGGAGATCAGGCATCTTCTCTGTGAGATCCCACT
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT
 25 GACCTTCTGATTCCCTCTCTTGCTGCTATACTGGCCTCCTATACACAAATTCTACTCACTG
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTACCTGCTCTTCCACCT
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGCCAGTTCTCTCC
 ACAGCACCAGACAAGACAACATCATCTCTGTTTCTACACAATTGTCACTCCAGCCCTGAA
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTGATGCGGGCCTTGAGGAGGGTCTGGG
 30 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

AOLFR108 sequences:

MCSFFLCQTGKQAKISMGEENQTFVSKFIFLGLSQDLQTOILLFILFLIHYLLTVLGNQLIILIFLD
 SRLHTPMYFFLRNLSFADLCFSTSIVPQVLVHFLVKRKTISFYGCMTQIIVFLVGCTECALLAV
 35 MSYDRYVAVCKPLYYSTIMTQRVCLWLSFRSWASGALVSLVDTSTFTFLPYWGQNIINHYFCE
 PPALLKLASIDTYSYMAIFSMGVVILLAPVSLILGSYWNHISTVIQMQSGEGRKAFSTCGSHLI
 VVFLFYSGIFTYMRPNKTTKELDKMISVFYTAFTPMLNPIIYSLRNKDVKGALRKLVRKRC
 FSHRQ (SEQ ID NO: 199)

40 ATGIGTCTTTTTTCTTGTCACAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA
 ACCAAACCTTTGTGTCCAAGTTTATCTTCTGGGTCTTTCACAGGACTTGACAGCCAGAT
 CCTGCTATTTATCCTTTTCTCATCATTTATCTGCTGACCGTGCTTGGAAACCAGCTCATCA
 TCATTCTCATCTTCTGGATTCTCGCCTTCACACTCCCATGTATTTTTTCTTAGAAATCTCT
 CCTTTCAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTGGTTCCTTCTGGTA
 45 AAGAGGAAAACCATTTCTTTTTATGGGTGTATGACACAGATAATTGTCTTCTTCTGGTTG
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCATGACCGGTATGTGGCTGTCTGCAA
 GCCCTGTACTACTTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTTCAAGTCTCT
 GGGCAGTAGGGGCACTAGTGTCTTAGTAGATACCAGCTTTACTTTCCATCTTCCCTACTG
 GGGACAGAAATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC
 50 ATAGACACTTACAGCACAGAAATGGCCATCTTTTCAATGGGCGTGGTAATCCTCCTGGCCC
 CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT
 GGGGAAGGGAGACTCAAGGCTTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGTCTCTT
 CTATGGGTGAGGAATATTCACCTACATGCGACCAAACTCCAAGACTACAAAAGAACTGGA
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC
 55 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAACTAGTTGGGAGAAAGTGCTTCTCT
 CATAGGCAGTGA (SEQ ID NO: 200)

AOLFR109 sequences:

- MLRNGSIVTEFILVGFQSSSTSTRALLFALFLALYSLTMAMNGLIIFITSWTDPKLNSPMYFFLG
HLSLLDVCFITTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGVAECILLAFMAYDRYVAICY
5 PLNYVPIISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
WAIFADAIVVILSPMVLTVTSYVHILATILSKASSGRGKTFSTCASHLTVVIFLYTSAMFSYMN
PHSTHGPDKDKPFSLLYTIITPMCNIYISFRNKEIKEAMVRALGRTRLAQPSV (SEQ ID NO:
201)
- 10 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTTCAGCAGAGCTCCA
CTTCCACACGAGCATTGCTCTTTGCCCTCTTCTTGGCCCTCTACAGCCTACCATGGCCATG
AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
TCTTCTCGGCCATCTGTCTCTGCTGGATGTCTGCTTCATCACCCTACCATCCACAGATG
TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
15 ACTTTGTCTTCTGTGTGGTGTGGCCGAGTGCATCCTCTTGGCTTTCATGGCCTATGACCGT
TATGTTGCTATCTGCTACCCACTTAACTATGTCCCGATCATAAGCCAGAAAGGTCTGTGTCA
GGCTTGTGGGAACCTGCCTGGTTCTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTT
ATTCCGAGAGCCCTTCCGCAGAGACAACACATAGAAAGCTTCTTCTGTGAGGCCCCCATA
GTGATTGGCCTCTCTTGTGGGGACCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA
20 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACTTCTATGTGCACATCCTGGCCACC
ATCCTCAGCAAAGCCTCCTCCTCAGGTGCGGGGAAGACTTTCTCTACTTGTGCCTCTCACC
TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTTACATGAACCCCCACAGCACA
CATGGGCCTGACAAAGACAAACCTTTCTCCTCCTGTACACCATCATTACCCCCATGTGCA
ACCCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG
25 GAAGAACCAGGCTGGCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

- MKIANNVTVVTEFILLGLTQSQDIQLLVFVLILIFYLILPGNFLIIFIRSDPGLTAPLYLFLGNLAFL
DASYSFIVAPRMLVDFELSEKKVISYRGCTQLFFLHFLGGGEGLLLVMAFDRIYAIACRPLHCST
30 VMNPRACYAMMLALWLGGFVHSIIQVVLLRLPFCGPNQLDNFFCDVRQVIKLA CTDMFVVEL
LMVFNSGLMTLLCFLGLLASYAVILCHVRRASEGKNKAMSTCTTRVIIIIMFGPAIFYMCPF
RALPADKMVSLFHTVIFPLMNPMTYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:
203)
- 35 ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
AAGATATTAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCTCCTCCGTGA
AATTTTCTCATTATTTTACCATAAGGTGACACCTGGGCTCACAGCCCCCTCTATTTATT
TCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCATTGTGGCTCCAGGATGTTGG
TGGACTTCCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT
40 CTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC
ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
TGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCCTC
CGCTTGCTTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCGACAGGTCA
TCAAGCTGGCTTGCACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
45 GATGACACTCCTGTGCTTTCTGGGGCTTCTGGCTTCTATGCAGTCATCCTCTGCCATGTTT
GTAGGGCAGCTTCTGAAGGGAAGAACAAAGGCCATGTCCACGTGCACCACTCGTGTCTATTA
TTATACTTCTTATGTTTGGACCTGCTATCTTCATCTACATGTGCCCTTTTCAGGGCCTTACCA
GCTGACAAGATGGTTTCTCTCTTTTACACAGTGATCTTTCCATTGATGAATCCTATGATTTA
TACCCTTCGCAACCAGGAAGTGAAAACCTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
50 TGTCAAGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

- MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCILHSILFLIYLCALM
GNVLIIMITLDDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSIHNNSISFLGCVSQVFLLS
55 ASAELLLLTVMSFDRYTAICHPLHYDVMRSTCVQRATVSWLYGGLIIVMHTAGTFSLSYCG
SNMVHQFFCDIPQLLAISCSENLIREIALILINVVLDFFCCFVMIITYVHVSTVKKIPSTEGQSKAY

SICLPHLLVVFLSTGFIAYLKPASESPSILDAVISVFYTMLPPTFNPIIYSLRNKAIKVALGMLIKG
KLTKK (SEQ ID NO: 205)

5 ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
TTTCCTGCAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA
TGGGGTTTTCTACCAATAAAAAATATGTGCATTTTGCATTTCGATTCTCTTCTTGTGATTAT
TTGTGTGCCCTGATGGGGAATGTCCTCATTATCATGATCACAACCTTGGACCATCATCTCC
ACACCCCCGTGATTTCTTCTTGAAGAATCTATCTTCTTGGATCTCTGCCTTATTTTCAGTC
ACGGCTCCCAAATCTATCGCCAATTCCTTTGATACACAACAACCTCCATTTTATTCTTGGCTG
10 TGTTTCCCAGGCTCTTTTGTGCTTTCTTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA
TGCTTTTGACCGCTATACTGCTATATGTACCCCTCTGCACTATGATGTCATCATGGACAGG
AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC
ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT
GACATTTCCCAGTTATTAGCTATTTCTTGCTCAGAAAATTTAATAAGAGAAAATTGCACTCA
15 TCCTTATTAAATGTAGTTTGGATTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC
GTCTTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT
GCCTTCCACACTTGCTGGTTGTGTTATTTCTTCCACTGGATTCAATTGCTTATCTGAAGCCA
GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCCC
AACCTTTAATCCCATATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
20 TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

MKFWHGFSSHLNPMFSSFLYLSLPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP
SVVTCSSSQSSDWMQLCTHLCTTSLVFFPSWSCGILPLSLRCLIFSRRKPFLLQDASFRPTSS
25 TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTILCAKMAAACWTCGFLCPISEVILASQLPF
CAYNEIQHIFCDFPPLLSLACKDTSANILVDFAINAFILITFFFIMISYARIIGAVLKIKTASGRKK
AFSTCASHLAVVLIFFGSIIFMYVRLKKSYSLTLDRTLAIVSVLTPMVNPIIYSLRNKEIKAIKR
TIFQKGDKASLAHL (SEQ ID NO: 207)

30 ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
AAAAAGTCTCACITGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTCTGTGTTCTGGCTGCTGTGGACATTGTTA
35 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
40 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGTCTGATTGGTTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAGCACATGTGGCTCCCATGTGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCCAAGTCCTGC
45 TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
CAAACAACGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
CTGGGTTTCATGA (SEQ ID NO: 208)

AOLFR114 sequences:

50 MERINHNTSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVTITGNLLIILAIRFNPHLQTPMYFFLSFLS
LTDICFTTSVVPKMLMNFLEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDYVAVCDPF
HYVTTMSHHHCVLLVAFSCSPHLHSLHLLNRLTFCDNSVHHFLCDLSPVLKLSCSSIFVN
EIVQMTEAPIVLVTRFLCIAFSYIRILTTVLKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLQP
PSTYAVKDHVATIVYTVLSSMLNPFIIYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

55

ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC
 GGCCTGAGGACCAAAAGACACTCTTTGTTCTCTTCTCATCGTGACCTGGTCACCATAAC
 AGGGAACCTGCTCATCATCCTGGCCATTGCTTCAACCCCATCTTCAGACCCCTATGTATT
 TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCAAGATG
 5 CTGATGAACTTCCTGTCAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT
 ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG
 CTATGTGGCCGTCTGTGACCCTTTCCACTATGTCACCACCATGAGCCACCACCACTGTGTCC
 TGCTGGTGGCCTTCTCCTGCTCATTTCTCACCTCCACTCACTCCTGCACACACTTCTGCTG
 AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCCTTTCTCTGTGACCTCAGCCCTGT
 10 GCTGAAATTGCTCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT
 ATTGTTTTGTTGACTCGTTTTCTCTGCATTGCTTTCTCTTATATACGAATCCTCACTACAGT
 TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTTACCTCA
 CCGTGGTGACGCTCTTTTATGGAAGCATCTTCTGTGTCTATTTACAGCCCCCATCCACCTAC
 GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTTGTCATCCATGCTCAATCCTT
 15 TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA
 GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

MEGFYLRSHLQGMGKPRVQNQTTVSDFLLLGLSEWPPEEQPLLFGIFLGMVLTVMVGNLLII
 20 LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD
 NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLTNCPALMHTLLTRVAFCAQK
 AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFTVPLLLIVFSYVRIFWAVFVISSPGGRWKA
 FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLNRNMDKEALG
 KLFVSGKTFFL (SEQ ID NO: 211)

25 ATGGAAGGTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA
 GTGAACCAAACCACTGTTTCAGACTTCCTCCTTAGGACTCTCTGAGTGGCCAGAGGAGC
 AGCCTCTTCTGTTTGGCATCTTCTTGGCATCTACCTGGTCACCATGGTGGGGAACCTGCTC
 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTCTTTCTGGCCAA
 30 CCTGTCAATTAAGTATGCTGCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAACATTC
 ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGACAGCTATATTTCTCCTTATG
 TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT
 GCCAACCACTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGCACTAATGCTGGGTGT
 GTGCTGGGTGCTAACCAACTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
 35 TTCTGTGCCCAGAAAGCCATCCCTCATTTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC
 CTGCTCAGATACCCATGTAAACGAGCTGATGATCATCACCATGGGCTTGCTGTTCCTCACT
 GTTCCCCTCTGCTGATCGTCTTCTCCTATGTCCGATTTTCTGGGCTGTGTTGTCTATCTC
 ATCTCCTGGAGGGAGATGGAAGGCCTTCTACCTGTGGTTCTCATCTCACGGTGGTTCTG
 CTCTTCTATGGGTCTCTTATGGGTGTGATTTACTTCTCCATCAACTTACTCTACAGAGAG
 40 GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATCCACGCTAAACCCATTCAATTTAT
 AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTTGTCAGTGAAAAACA
 TTCTTTTTATGA (SEQ ID NO: 212)

AOLFR116 sequences:

45 MDEANHSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN
 LSIINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH
 YLTIMNPQRCLFLVISWIIHHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV
 TANSGFISLASFLIHSYIFILVTVQKKSSGGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPPTSHLD
 KFLAIFDAVITPVLPVITYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

50 ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTCCTGGGACTCTCTGACTCGC
 GGAAGATCCAGCTCCTCCTCTTCTCTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA
 AATCTCCTCATTGTGCTAACTGTGACCTCTGACCCTCGTTTACAGTCCCCCATGTACTTCT
 GCTGGCCAACCTTTCCATCATCAATTTGGTATTTTGTTCCTCCACAGCTCCCAAGATGATTT
 55 ATGACCTTTTACAGGAAGCACAAAGACCATCTCTTTTGGGGGCTGTGTAGTTACAGATCTTCTT
 TATCCATGCAGTTGGGGGAAGTGAAGTGGTGCTCATAGCCATGGCTTTTGACCGATAT

GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT
 TTTTAGTCATTTCCCTGGATTATAGGTATTATTCACCTCAGTGATTTCAGTTGGCTTTTGTGTGA
 GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCCCTCGATTTAT
 CAAACTGGCTTGCATAGAGACCTACACATTGGGATTTCATGGTTACTGCCAATAGTGGATTT
 5 ATTTCTCTGGCTTCTTTTAAATTCTCATAATCTCTTACATCTTTATTTTGGTGACTGTTTCAG
 AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTCAGCTCATGTCATTGTGG
 TGGTTTTGGTCTTTGGGCCATTAATCTTTTCTATATTTTCCATTTCCCACATCACATCTTG
 ATAAATTCCTTGCCATCTTTGATGCAGTTATCACTCCCGTTTGAATCCAGTCATCTATACT
 10 TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC
 AGTAAAATCTTTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLVISRLLLAMTLGNSTEVTEFYLLGFGA
 QHEFWCILFIVFLLIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT
 15 EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRTVCIRLVAGSYI
 MGSINASVQTGFTCSLSFCKSNSINHHFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS
 YYIMATILKMSSSAGRKKSFSTCASHLTAVTIFYGTLSYMYLQSHSNNSQENMKVAFIFYGTVI
 PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215)

20 ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAGTGACTTGAAATATA
 GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTTCTGGGTCTTCTCTTGGTC
 ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC
 TTCTGGGATTTGGTGCCAGCATGAGTTTTGGTGTATCCTCTTCATTGTATTCCTTCTCATC
 TATGTGACCTCCATAATGGGTAATAGTGAATAATCTTACTCATCAACACAGATTCCAGAT
 25 TTCAAACACTCACGTACTTTTTCTACAACATTTGGCTTTTGTGATATCTGTTACACTTCT
 GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAAGAAAGAATTTGATATTATTTTCAGG
 GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCCTGGCT
 ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCTTCACTATACTGTAATCATGT
 CCCGAACAGTCTGCATCCGTTTGGTAGCTGTTTCATACATCATGGGCTCAATAAATGCCTC
 30 TGTACAAACAGGTTTTACATGTTCACTGTCTTCTGCAAGTCCAATAGCATCAATCACTTTT
 TCTGTGATGTTCCCCCTATTCTTGCTCTTTCATGCTCCAATGTTGACATCAACATCATGCTA
 CTTGTTGTCTTTGTGGGATCTAAGTTGATATCACTGGGTTGGTCTGTCATCTTTTCTACAT
 CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCCTTCTCA
 ACATGTGCTTCCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT
 35 GCAGTCTCATTCTAATAATTCCCAGGAAAATATGAAAGTGGCCTTTATATTTTATGGCACA
 GTTATTTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT
 TAAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

AOLFR118 sequences:

40 MNHMSASLKISNSSKFQVSEFILLGFPPIHSWQHWLSLPLALLYLSALAANTLILIHWNPSLQQ
 PMYIFLGILCMVDMGLATTIIPKILAIWFDAKVISLPECFAQIYAIHFFVGMESGILLCMADFDRY
 VAICHPLRYPISVTSSLILKATLFMVLRNGLFVTPVPVLAQRDYCSKNEIEHCLCSNLGVTS
 CDDRRPNSICQLVLAWLGMGSDLSLILSYILILYSVLRNLNSAEAAAKALSTCSSHLTLILFFYTIV
 VVISVTHLTEMKATLIPVLLNVLHNIPPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID
 45 NO: 217)

ATGAATCATATGTCTGCATCTCTCAAATCTCCAATAGCTCCAAATTCAGGTCTCTGAGTT
 CATCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCTTGCA
 CTAATGTATCTCTCAGCACTTGCTGCAACACCCTCATCCTCATCATCTGGCAGAACCC
 50 TTCTTTACAGCAGCCCATGTATTTTCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG
 CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTTGTATGCCAAGGTTATTAGCCTC
 CCTGAGTGCTTTGCTCAGATTTATGCCATTACCTTCTTGTGGGCATGGAGTCTGGTATCCT
 ACTCTGCATGGCTTTTGTATAGATATGTGGCTATTTGTACCCTCTTCGCTATCCATCAATTG
 TCACCAGTTCCTTAATCTTAAAAGCTACCCTGTTTCATGGTGCTGAGAAATGGCTTATTTGTC
 55 ACTCCAGTGCCTGTGCTTGCAGCACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT
 GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT

TTGCCAGTTGGTTCTGGCATGGCTTGGAAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
TATATTTTATTCTGTACTCTGTACTTAGACTGAACTCAGCTGAAGCTGCAGCCAAGGCC
TGAGCACTTGTAGTTCACATCTCACCCTCATCCTTTTCTTTTACACTATTGTTGTAGTGATT
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC
5 ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAGAAGCTTAG
GGCAGCCTTCCAAAAGGTGCTGTTTGCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
218)

AOLFR119 sequences:

10 MPLFNSLCWFPTIHVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP
MYFFFGHALSLIDLLTCTTLPNALCIFWFSLEKINFNACLAQMFFVHGFTGVESGVLMLMALD
RYIAICYPLRYATTLTNPIIAKAEATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL
SCASIKVNVYGLMVALLIGVFDICISLSYTLILKAAISLSSSDARQKAFSTCTAHISAIHTYVPA
15 FFTFFAHRFGGHTIPPSLHIIVANLYLLPPTLNPIVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID
NO: 219)

ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT
TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCCTCTGCACA
ATGTACATCATCTTCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTTATTATGAGGAGTC
20 CTTACATCATCCGATGTATTTTGTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG
CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTTCA
ATGCTTGCTTGGCCCAGATGTTCTTTGTTCATGGGTTACAGGTGTGGAGTCTGGGGTGCT
CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCTTTGCGTTATGCTACCACAC
TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCTGAGGGGTGTATTGCTGAT
25 GATTCCTTTCCCATCTTGGTTAAGCGTTTGCTTTCTGCCAAAGCAATATTATCTCCCAT
CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTGACATTTGTTGTATATCTTTGTCTT
ACACTTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT
CAGCACCTGCACCTGCCATATATCTGCCATCATCATCACCTATGTTCCAGCATCTTTCACCT
30 TCTTTGCCACCGTTTTGGGGGACACACAATTCCCCCTTCTCTTCACATCATTGTGGCTAAT
CTTTATCTTCTTCTCCCCCAACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT
ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

AOLFR120 sequences:

35 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAILLVGLDHRRLRRPMYF
FLTHLSLEIWIYTSVTPKMLAGFIGVDGKNISYAGCLSQLFIFTLGATECFLLAAMAYDRY
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPILPIYLLSQLTFCGPNVIDHFSCDASPLLALS
CSDVTWKETVDFLVSLAVLLASSMVIAVSYGNIWVTLHRSAAERWKAFTCAHLLTVVSLF
40 YGTLFFMYVQTKVTSSINFNKVVSVFYSVVTMLNPLIYSLRNKEVKGALGRVFSLNFWKQG
(SEQ ID NO: 221)

ATGCAACCATATACCAAAAAGTGGACCCAGGTAAGTGAATTTGTCATGATGGGCTTTGCTG
GCATCCATGAAGCACACCTCCTCTTCTTCATACTCTCCTCACCATGTACCTGTTACCTTG
GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCAACCGACTACGGAGACCCATGT
45 ATTTCTTCTGACACACTTGTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG
ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAATATCTCTTATGCTGGTTGCCTAT
CCCAGCTCTTCATCTTCACTTTCTTGGGGCAACTGAGTGTTCCTACTGGCTGCCATGGCC
TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCTGGGGCAC
CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCTCACACCCATCTTGCCAATCT
50 ACCTCTTGTCTCAGCTAACATTTTGTGGCCCAAATGTCATTGACCATTTCTCCTGTGATGCC
TCACCTTGCTAGCCTTGTCTGTCTCAGATGTCACTTGGAAGGAGACTGTGGATTTCTGG
TGCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCAATTGCTGTGTCTATGGCAACATCGTC
TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTGTGCAG
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTTCTTTATGTATGTCCAGACCAAG
55 GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTACGCCCAT

GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTCGAGTC
TTTTCTCTCAACTTTTGAAGGGACAGTGA (SEQ ID NO: 222)

AOLFR121 sequences:

5 MKRKNFTEVSEFIFLGFSSFGKHQITLFVVFLT VYILTLVANIIVTIIICIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFVILATNNCFLLTAMGYDRYVAICRPLRY
TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAMFNLPFCGTVVDHFFCDIYPVMKLSCIDTTINEII
NYGVSSFVIFVPIGLIFISYVLVISSILQIASAEGRKKTATCVSHLT VVTVHCGCASIA YLKPSES
SIEKDLVLSVYTHITPLLNPVVYSLRNKEVKDALCRVVRNIS (SEQ ID NO: 223)

10 ATGAAGAGAAAGAACTTCACAGAAGTGTCAGAATTCATTTTCTTGGGATTTTCTAGCTTTG
GAAAGCATCAGATAACCCTCTTTGTGGTTTTCTAACTGTCTACATTTTAACTCTGGTTGCT
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTTCTT
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGACACACTGGTCATTGTGCCACGAATGCTT
15 TTGAGCCTCATTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT
TTTTGTATCTTGGCCACTAATAATGCTTCTCTGCTTACTGCAATGGGGTATGACCGCTATG
TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCAGCT
GGTGTGTGGGTCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTT
AATTGCCGTTCTGTGGCACAGTGGTAGACCACTTCTTTGTGACATTTACCCAGTCATGA
20 AACTTCTTGCATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAGTTCATTGT
GATTTTGTGCCCATAGGCCTGATTTTATCTCCTATGCTTGTGTCATCTCTCCATCCTTC
AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCACTGT
GGTTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA
ATAGAAAAAGACCTTGTTCTCTCAGTGACGTACCCATCATCACTCCCTTGCTGAACCTG
25 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
ATATTTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

MEWENQTLVEFFLKGHSVHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
30 SFLDICYTTSIPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
YPIIMSKNAYVPMVAVGSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCEILAVMKLACADISGN
EFLMLVATILFTLMPLLLVISYSLISSLKIHSSSEGRSKAFSTCSAHLTVVIIFYGTILFMYMKPKS
KETLNSDDL DATDKIISM FYGVMT PMMNPLIYSLRNKDVKEAVKHLPNRRFFSK (SEQ ID NO:
225)

35 ATGGAATGGGAAAACCAAACCATTTCTGGTGGAATTTTTTCTGAAGGGACATTCTGTTACCC
CAAGGCTTGAGTTACTCTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCCTCACCTTCACACCCCTATGCTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG
40 TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCTTTTCTGGCTGTGCAGTGCAGATGTTCTT
GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG
TGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT
GGCTGTGGGTCTCTGTTTGCAGGGATTGTCAACTCTGCAGTACAAACTACATTTGTAGTA
CAATTGCCCTTCTGCAGGAAGAATGTCAATCAATTTCTCATGTGAAATTCTAGCTGTGCT
45 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCCTCATGCTTGTGGCCACAATATTG
TTCACATTGATGCCACTGCTCTTGATAGTTATCTTACTCATTAATCATTTCAGCATCCT
CAAGATTCACTCCTCTGAGGGGAGAAGCAAAGCTTTCTCTACCTGCTCAGCCCATCTGACT
GTGGTCATAATATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA
CACTTAATTCAGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT
50 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT
AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

MYRFTDFDVSNISYILNHVLFYTTQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL
55 IMYMIILLGNSLLIITILDSRLHTPMYFFLGNL SFLDICYTSSSIPMLIIFMSERKSISFIGCALQM
VVSLGLGSTECVLLAVMAYDHYVAICNPLRYSIMNGVLYVQMAAWSWIIGCLTSLQLTVLT

MMLPFCGNNVIDHITCEILALLKLVCSDITINVLMITVNTIVSLVILLLLIFISYVFLSSILRINCAE
GRKKAFSTCSAHSIVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV
KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

- 5 ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT
CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
GACTGAATTCTTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCTGC
TCTGCCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC
10 TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGAAACCTCTCATTCTTGACAT
CTGTTACACATCCTCATCCATTCTCCAATGCTTATTATATTATGTCTGAGAGAAAATCCA
TCTCCTTCATTGGCTGTGCTCTGCAGATGGTGTGTCCCTTGGCTTGGGCTCCACTGAGTGT
GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
CCATCATCATGAACGGAGTGTGTATGTGCAAAATGGCTGCATGGTCTGGATCATAGGCTG
TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGAATAATGTC
15 ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACCTGTTTGTTCAGATATCACCAT
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT
TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG
AAAGCCTTCTCTACCTGTTTCAGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT
TTTTATGTACATGAAACCCAAGTCAAAGAACACTAATACATCTGATGAGATTATTGGGCTG
20 TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
TCAAAGAGGCTGTAAAGAAAGTCCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ
ID NO: 228)

AOLFR124 sequences:

- 25 MNHSVVFTEFILLGLTKKPELQGHFLFFLVYLVAFLGNMLIIAKIYNNTLHTPMYVFLTLAVV
DIICTTSIPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFITMAYDRYAICFPLHYST
VMNHHMCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPPLALSCSPVRINEV
MVYVADITLAIGDFILTCISYGFIVAILRIRTVGKRAKAFSTCSSHLTVVTLYSPVIYTYIRPASS
YTFERDKVVAALYTLVPTLNPMVYSFQNRMQAGIRKVFAFLKH (SEQ ID NO: 229)
- 30 ATGAATCACAGCGTTGTAAGTGAAGTTCATTATTCTGGGCCTCACAAAAAGCCTGAAGTCC
AGGGAATTATCTTCTCTTTTCTCATTGTCTATTGTGGCTTTCTCGGCAACATGCTC
ATCATCATTTGCCAAAATCTATAACAACACCTTGACATACGCCCATGTATGTTTTCTTCTGAC
ACTGGCTGTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
35 GCTAACATCAGAAAATACCATTTTCATATGCAGGCTGCATGTCCCAGCTCTTCTGTTTACA
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA
TTTGTCTTCCCTCTTTCATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
CTTTCTGTGGGCCAAACACCATGACCACTTCTTCTGTGAGATACCCCATGCTGGCTTTG
40 TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCCTGGCCA
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC
CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG
ACCCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA
AAGAGACAAGGTGGTAGCTGCACTCTATACTCTGTGACTCCCACATTAAACCCGATGGTG
45 TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA
CACTAG (SEQ ID NO: 230)

AOLFR125 sequences:

- 50 MTNQTMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAMYFFLRH
LSFLDLCLISATVPKSILNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSVDYRVAIICPLHC
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSNLFYGSDELHQFFCDVPALLKLTCSKEHAI
ISVSAIGVCYAFSCLVCIVSVSYVYIFSAVLRISQRQRQSKAFSNCVPHLIVVTVFLVTGAVAYL
KPGSDAPSILDLLVSFYSVAPPTLNPVTYCLKNKDIKSALS KVLWNVRSSGVMKDD (SEQ ID
NO: 231)

55

ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC
 TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA
 GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTCTCCG
 ACATTTGCTCTTCTTAGACCTGTGTCTCATTTCTGCCACAGTCCCCAAATCCATCCTCAACT
 5 CTGTCGCCTCCACTGACTCCATCTCCTTCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA
 CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCCTATGACCGCTATGCTGCCA
 TCTGCTGCCCCCTACACTGTGAGGCTGTCATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC
 TCTGTCTGGCTCAACAGAGGGGCTTGGGACTCTGTACACAGCTGGAACATTCTCTCTG
 AATTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT
 10 CACTTGTCTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA
 TTTTCATGTTTAGTTTGCATTGTAGTTTCTATGTGTACATTTTCTCTGCTGTGTTAAGGAT
 ATCACAGAGACAGAGACAAATCCAAAGCCTTTTCCAACCTGTGTGCCTCACCTCATTGTTGTC
 ACTGTGTTTCTTGTAAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
 TCTAGACTTGTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTTGAACCTGTTATCT
 15 ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCTGTGGAATGTTAGAA
 GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

MFLYLFCFQRTCEEMEEENATLLTEFVLTGFLHQPDKIPLFLAFLVLYLITIMGNLGLIVLIW
 20 KDPHLHPMYLFLGSLAFVDASLSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
 ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGGLLHALIHEAFSRLTFCNSNIIHFYCDII
 PLLKISCTDSSINFLMVIFAGSVQVFTIGTILISYTIILFTILEKKSIRKAVSTCGAHLISVSLY
 YGPLTFKYLGASAPQADDQDMMESLFTYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
 NO: 233)

25 ATGTTCCCTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
 ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTTACATCAACCTGACTGTAAAAT
 ACCGCTCTTCTGGCATTCTTGGTAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA
 TTGTTCTCATCTGGAAGACCCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA
 30 GCCTTTGTGGATGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTCTTAG
 CTAAGAGTAAGATGATATCTCTCTGAAATGCATGGTACAATTTTTTCCCTTGTAACCACT
 GTAACCACAGAATGTTTTCTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTTGCA
 AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTGAGCTATTAGTCTTGTC
 TTTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTCATTGAGTTAACCTTCTG
 35 TAATTTCAACATAATACAACACTTTTACTGTGACATTATCCATTGTTAAAGATTTCTGTGA
 CTGATTCCTCTATTAACCTTTCTAATGGTTTTTATTTTCGAGGTTCTGTTCAAGTTTTTACCA
 TTGGAATATTCTTATATCTTATACAATTATCCTCTTTACAATCTTAGAAAAGAAGTCTATC
 AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTACT
 ATGGCCCCCTCACCTTCAAATATCTGGGCTGTGCATCTCCGAAGCAGATGACCAAGATAT
 40 GATGGAGTCTCTATTTTACACTGTGATGTTCTTTATTTAAATCCCATGATCTACAGCCTGA
 GAAACAAGCAAGTAATAGCTTCATTCACAAAAATGTTCAAAGCAATGTTTAG (SEQ ID
 NO: 234)

AOLFR127 sequences:

45 MSNEDMEQDNTLLTEFVLTGLTYQPEWKMPFLVFLVLYLITIVWNLGLIALIWNPDQLHIPM
 YFFLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY
 VAICKPLLYPVIMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIIHFYCDIPLFMISCTD
 PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLISVSLYGYPLIF
 MYLRPASQADDQDMIDSVFYTHIPLNPIIYSLRNKQVIDSF TKMVKRVN (SEQ ID NO: 235)

50 ATGTCGAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTTGTCTCACA
 GGACTTACATATCAGCCAGAGTGGAATAATGCCCTGTTCTTGGTGTCTTGGTGTATCTATC
 TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACTTCAC
 ATCCCCATGTACTTTTTTCTTGGGAGTTTATGCTTTGTTGATGCTTGGATATCTTCCACAGT
 55 AACTCCCAAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC
 ATGATTCAATTTTTTCTTTGCATTTGGTGAACTACAGAATGTTTTCTTGGCAACAAT

GGCATATGATCGCTATGTAGCCATATGCAAAACCTTTACTATATCCAGTGATTATGAACAAT
 TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCCTCCATGCCTTAATTCA
 TGAAGTCCTTATATTAGATTAAACCTTCTGCAATTCTAACATAATACATCATTTTTACTGTG
 ATATTATACCACTGTTTATGATTTCTGTACTGACCTTCTATTAATTTTCTAATGGTTTTTA
 5 TTTTGTCTGGCTCAATTCAGGTATTCACCATTGTGACAGTTCTTAATTCTTACACATTGCT
 CTTTTACAATCCTAAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG
 GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGATTTGCGCCCT
 GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACAATCATAATTC
 CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAAACAAGTAATAGATTCATTCACAAA
 10 AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

METQNLTVVTEFILLGLTQSQDAQLLVFVLVLFYLLPGLNFIIFTIKSDPGLTAPLYFFLGNL
 LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMFAFDRIYACRPLHY
 15 STIMNPRACYALSLVLWLGGFHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL
 LMVSNGLLSLLCFLGLASYAVILCRIREHSSEKSKAISTCTTHIIIFLMFGPAIFIVTCPFQAFP
 ADKVVSILFHTVIFPLMNPVITYTLRNQEVKASMRKLLSQHMFC (SEQ ID NO: 237)

ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC
 20 AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTATCATCTCCCTGGA
 AATTTCCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTT
 TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCATTGTGGTTCCAGGATGTTG
 GTGGACTCCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTT
 TCTTGCATTTTCTTGGAGCGGGAGAGATGTTCTCCTCGTTGTGATGGCCTTTGACCGCTAC
 25 ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT
 TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
 CACTTGCTTTCTGTGGCCCAACAGCTCGATAAATTCTTCTGTGATGTTCCACAGGTCAT
 CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG
 CTCAGCTCCTGTGCTTCTTGGGCTTCTGGCCTCCTATGCAGTCATCCTCTGTGCTATAAG
 30 GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCATATTATCATT
 ATATTTCTCATGTTTGACCTGCTATTTTCATCTACACTTGCCCTTCCAGGCTTTCCAGC
 TGACAAGGTAGTTTCTCTTTTCCATACTGTCATCTTCTCTTGTGATGAACCCTGTTATTTATA
 CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG
 CTGA (SEQ ID NO: 238)

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AOLFR129 sequences:

MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLFALFSVI
 YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
 QIFLLHLLGGVEMVLLVSMFAFDRIYVAICKPLHYMTIMNKKVCVLLVVTWLLGLHSGFQIPF
 40 AVNLPFCGPNVDSIFCDLPLVTKLACIDIYFVQVVIVANSGLSCLFILLISYSLILITIKNHSPT
 GQSKARSTLTAHITVVILFFGPCIFYIWPFGNHSVDKFLAVFYTIITPILNPIYTLRNKEMKISMK
 KLWRAFNVSREDT (SEQ ID NO: 239)

ATGGCTCTTTATTTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTTCTCTACAGG
 45 TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAACTATTAATCAATCTCAAGTGTC
 AGAATTCATTTTGTGGGACTGACCACTCCAGGATGTAGAGTTTCTTCTTTGCCCTCT
 TCTCGGTATCTATGTGGTCACAGTTTTGGGTAACTTCTTATTATAGTCACAGTGTTTAAAC
 ACCCTAACTGAATACTCCCATGTATTTTCTCCTTGGTAATCTCTCTTTGTAGATATGAC
 CCTTGCTTCTTTGCCACCCCTAAGGTGATTCTGAACCTGTTAAAAAAGCAGAAGGTAATT
 50 TCTTTTGTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGTTGAAATGGT
 ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCTACACTACATG
 ACCATCATGAACAAGAAGGTATGTGTTTTGCTTGTAGTGACCTCATGGCTCTTGGGTCTCC
 TTCACTCAGGGTTTCAGATACCATTTGCTGTGAACCTTGCCCTTTTGTGGTCCCAATGTGGTA
 GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCTGTATAGACATATATTTTGT
 55 ACAGGTAGTCATTGTTGCCAAGAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGT
 TCTCCTACAGTCTGATCCTCATAACCATTAAAGAACCACTCTCCTACTGGGCAATCTAAAGC

CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTCTTTGGCCCATGCATCTTTA
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTTATACCATC
ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

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AOLFR131 sequences:

MASTSNVTELTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
LVEISYSSTIAPKFIIDLLAKIKTISLEGCLTQIFFHFFGVAEILLIVVMAYDCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSIIQLVIIQLPFCGPNVIDHYFCDLQPLFKLACTDTFMEGVIVLA
NSGLFSVFSFLILVSSYIVILVNLNRNHAEGRHKALSTCASHITVVILFFGPAIFLYMRPSSFTED
KLVAVFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKNPGRE (SEQ ID NO: 241)

10

ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG
TGCAGAGTGTATGCTTTGTGGTGTCTTCCCCGTGTACCTTGCCACGGTGGTGGGCAATGG
CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCTTA
GCTGCCTGTCTTGGTGGAGATCAGTTATTCTCCACTATCGCCCCTAAATTCATCATAGAC
TTACTTGCCAAGATTAAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA
CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGTATGGCCTATGATTGCTACGTGGCC
ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTACCTTCTGGTGGC
TGTTTCTGGCTGGGGGGCTTTTGTCACTCCATAATTGAGATTCTCGTTATCATCCAATTGC
CCTTCTGTGGTCCCAATGTGATTGACCACTATTCTGTGACCTCCAGCCTTTATTCAAGCTT
GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTTGGCCAACAGTGGATTATTCTCTG
TCTTCTCCTTCTCATCTTGGTGTCTCTTATATTGTCACTTCTGGTCAACTTGAGGAACCAT
TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
TGTTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTTCACTGAAGATAAA
CTTGTTGGCTGTATTCTACACGGTCATACCCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA
GGGAGTGA (SEQ ID NO: 242)

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30 **AOLFR132 sequences:**

MVATNNVTEIIFVGFSSQNWSEQRVISVMFLMYTAVVLGNGLIVVTILASKVLTSPMYFFLSYL
SFVEICYCSVMAPKLIFFSFIKRVISLKGCLTQMFSLHFFGGTEAFLLMVMAYDRYVAICKPL
HYMAIMNQRMCGLLVRIAWGGGLLHVSQGTFILFQLPFCGPNIMDHYFCDVHPVLELACADT
FFISLLIITNGGSISVVSFFVLMASYLIILHFLRSHNLEGQHKALSTCASHVTVVDLFFIPCSLVYIR
PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

35

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAAATTGGAGTG
AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG
CCTCATTTGTGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCCATGTATTTCTTTCTCA
GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTGTCATGGCCCCCAAGCTTATCTTTGAC
TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC
ATTTCTTTGGTGGCACTGAGGCCTTTCTCCTGATGGTGTATGGCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG
AGGATAGCATGGGGCGGGGGCCTGCTGCAATTCTGTTGGGCAAACCTTCCTGATTTTCCAGC
TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTTATTAGCCTGCTGATCATACCAATGGCGGCTCCATC
TCCGTAGTCAGTTTCTTCGTGCTGATGGCTTCTACCTGATCATCCTGCACCTCCTGAGAAG
CCACAACCTGGAGGGGCAGCACAAGGCCCTTCCACCTGTGCCTCTCATGTCACAGTTGTC
GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCCTCCCTGCAGA
CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT
TCAGGAATGCTGAAGTAAAAATGCCATGAGGAGATTTATTGGGGGAAAAAGTAATTTGA
(SEQ ID NO: 244)

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AOLFR133 sequences:

MTEFIFLVLPNQEVQRVCFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWWGCMAQLFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN

55

WQVCTVLVGIAWVGGMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFLIGLLIVAN
GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI
DKMVAVFYTVITAILNPVTYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

5 ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTTCTTGTACACAGCAATTGTGCTGGGGAATTCCTCATTGTGCTCACTGTC
ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCTCAGCTACCTCTCCTTCATGGA
GATCTGCTACTCCTCCGCTACAGCCCCAAACTCATCTCAGATCTGCTGGCTGAAAGGAAA
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCATCTTTTGGTGGCACTGA
10 GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCTCAGC
TACACCACCATCATGAACTGGCAGGTGTGTACTGTCTTGTAGGAATAGCATGGGTGGGA
GGCTTCATGCATTCCCTTTCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA
TGTGATCAATCACTATTTCTGTGACCTAGTTCCCTTCTCAAACCTGCCTGCTCTGACACCT
TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCCTGTCTGTGATCAGTTTGGGGT
15 CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTTCGCTGTGGTTATCTTGTCTTTGGGCCCTG
CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCCATAGACAAGATGGTGGCTGTGTTCT
ACACAGTGATAACCGCGATCCTGAACCCTGTCATCTACTCTCTGAGAAATGCTGAAATGAG
GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID
20 NO: 246)

AOLFR134 sequences:

MTTHLEVDNHTVTTRFILLGFPTRPAFQLLFFSIFLATYLLTLENLLILAIHSDGQLHKPMYFFL
SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC
25 NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFLAQLHYCGMPQINHYFCDISPLLNVSC
DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSM
LFTYARPKLMYAYNSNKVVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQNGAFS
S (SEQ ID NO: 247)

30 ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG
GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTTCTCCATTTTCTGGAACCTATCTG
CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
AGCCCATGTACTTCTTCTGAGCCACCTCTCCTTCTGAGATGTGGTATGTACAGTGCATC
AGCCCCAAGATGCTTGTTGACTTCTCAGTCATGACAAGAGTATTTCTTCAATGGCTGCA
35 TGACTIONACTTTACTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG
GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAACC
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA
GATGGTTTTTATAGCACAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG
ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT
40 CTTCTTGGCCCTCATGGTCATTGCTATTCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA
TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG
TGCCTCCCACTGACCGTCGTAATTCTCTTCTATTCCATGACACTTTTCACTATGCCCCTC
CCAAACTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTCTACACTGTCATTGTT
CCACTCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
45 AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTTCAGTAGTTAA (SEQ
ID NO: 248)

AOLFR135 sequences:

MIFPSHDSQAFTSVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIRT
50 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
AAMAYDRHAAICNPILLYSGTMSTALCTGLVAGSYIGGFLNIAHTANTFRLHFCGKNIDHFFC
DAPPLVKMSCTNTRVYEKVLGVVGFTVLSSILAILISYVNILLAILRIHSASGRHKAFSTCASHL
ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFRKATQTIQPO
T (SEQ ID NO: 249)

55

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT
 GCACCACCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT
 TCTATTTGGAGTGTTCCTGATGCTCTATTGTATAACCTTGTGAGGAAACATGACCTTGGTTA
 TCTTAATCCGAACTGATTCCCACTTGCATACACCTATGTACTTTTTCATTGGCAATCTGTCT
 5 TTTTGGATTTCTGGTATACCTCTGTGTATACCCCCAAAATCCTGGCCAGTTGTGTCTCAGA
 AGATAAGCGCATTTCCTTGGCTGGATGTGGGGCTCAGCTGTTTTTCTGTGTTGTAGCCT
 AACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC
 ATTGCTTTATTACAGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGCTGGCTCCTACA
 TAGGAGGATTTTGAATGCCATAGCCATACTGCCAATACATTCCGCCTGCATTTTGTGG
 10 TAAAAATATCAITGACCACTTTTCTGTGATGCACCACCATTGGTAAAAATGTCCTGTACA
 AACACCAGGGTCTACGAAAAAGTCTGCTTGGTGTGGTGGGCTTCACAGTACTCTCCAGCA
 TTCTTGCTATCCTGATTTCTATGTCAACATCCTCCTGGCTATCCTGAGAAATCCACTCAGT
 TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTCATGCTCTTCTA
 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCCACCTACTCCCTAGAGAGGGACAAA
 15 GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCTCTCATCTATAGCCTGAG
 AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
 A (SEQ ID NO: 250)

AOLFR136 sequences:

20 MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVTVVGNLGMILLIAVSPLLHTPMYYFL
 SSSLFVDFCYSSVITPKMLVNFLGKKNTILYSECMVQLFFFVVFVVAEGYLLTAMAYDRYVAIC
 SPLLYNAIMSSWVCSLLVLAFFLGLSALHTHSAMMKLSFCKSHIINHFCVDPLPLNLSCSNT
 HLNELLLFHAGFNTLVPTLAVAVSYAFILYSILHRISSEGRSKAFGTCSSHLMVAVIFFGSITFMY
 FKPPSSNSLDQEKVSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)
 25
 ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAACACAGCAAG
 CAGAGCTCCAGCTGCCCCCTCTTCCTCCTGTTCTCCTGGGAATCTATGTGGTCACAGTAGTGGG
 CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT
 TCCTCAGCAGCTTGCCTTCGTCGATTCTGCTATTCTCTGTCACTACTCCCAAAATGCTG
 30 GTGAACTTCTAGGAAAGAAGAATACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT
 TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA
 TGTGTCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCCTCATGGGTCTGCTCACTGC
 TAGTGCTGGCTGCCTTCTTCTTGGGCTTTCTCTCTGCCTTGACTCATAAAGTGCCATGATG
 AAAGTGCCTTTTGCAAATCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCCTCCT
 35 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTATCATTGCGGGGTTTA
 ACACCTTGGTGCCCACTAGCTGTTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT
 CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGAACATGCAGCTCTCATCTCATGG
 CTGTGGTGATCTTCTTGGGTCCATTACCTTCATGTATTTCAGCCCCCTTCAAGTAACCTCC
 CTGACCAAGGAGAAGGTGCTCTGTGTTCTACACACGGTGATCCCCATGCTGAACCTTT
 40 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA
 AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

MSPENQSSVSEFLLGLPIRPEQQA VFFALFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
 45 LALTDISFSSVTPKMLNMNMQTQHLAVFYKGCISQTYFFIFFADLDSFLITSMA YDRYVAICHPL
 HYATIMTQSQCVM LVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL
 NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYRTIIGLYFLP
 PSSNTNDKNIIASVIYTA VTPMLNPFYISLRNKDIKALRKLLSRSGAVAHACNLSTLGG (SEQ
 ID NO: 253)
 50
 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCTCCTCCTGGGCCTCCCCATCCGGC
 CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCTCCTGGGCATGTACCTGACCACGGTGCTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT
 TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
 55 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAAGGGATGCATTTACAGACATATT
 TTTTCATATTTTGTGCTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT

GTGGCCATCTGTCATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTCATGC
 TGGTGGCTGGGTCTGGGTTCATCGCTTGTGCGTGTGCTCTTTTGCATACCCTCCTCCTGGCC
 CAGCTTTCCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGGCCTGCT
 CAAGTTGTCCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA
 5 GCCATTATGCTTCCATTCCCTGTGCATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT
 CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCCACCTCTCA
 GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC
 CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
 TTCATTTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACCTTTGAGTAGG
 10 TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

MLNFTDVTEFILLGLTSRREWQVLFFIVFLVVIITVVGNI GMMMLLIKVSPQLNSPMYFFLSHLS
 FVDVWFSSNVTPKMLENLFSDKKTISYADCLAQCFFIALVHVEIFILAAIAFDRTVIGNPLLY
 15 GSKMSRGCIRLITFPYTYGFLTSLTATLWTYGLYFCGKIEINH FYCADPPLIKMACAGTFVKEY
 TMLLAGINFTYSLTVIISYLFILAILRMRSABGRQKAFSTCGSHPTAVIIFYGTLIFMYLRPTE
 ESVEQKGKMAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGGGAAT
 20 GGCAAGTTCTCTTCTCATCGTTTTTCTTGTGGTCTACATTATCACCGTGGTGGCAATATC
 GGCAATGATGTTGTTAATCAAGGTCAGTCTCAGCTTAACAGCCCCATGTACTTTTCTCA
 GTCACTTGTGCTTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAT
 CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTTAGCACAGTGTCTTCTTCTCAT
 TGCTCTTGTCCATGTGGAATTTTTATTCTTGTGCGATTGCCTTTGATAGATACACAGTGA
 25 TTGGAAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTGACTGATTAC
 TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT
 ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
 GGCCTGTGCGGGACCTTTGTAAAAGAATATACAATGCTCATACTTGCCGGCATCAACATTC
 ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTCGAAT
 30 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
 CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
 GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
 TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
 GTTAA (SEQ ID NO: 256)

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AOLFR139 sequences:

MGFPGIHSWQHWSLPLALLYLLALSANILIIINKEAALHQP MYYFLGILAMADIGLATTIMP
 KILAILWFNAKTISLLECFAQMYAIHCFVAMESSTFVCMAIDRYVAICRPLRYPSTITESFVKAN
 GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLS CDDRRINSINQVLLAWTLMGS
 40 DLGLILSYALILYSVLKLSPEAAASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNVL
 HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCCTGGCTCTGCTCT
 ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT
 45 GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC
 ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG
 AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT
 CTGCATGGCTATTGATAGATATGTAGCCATTTGTGACCGCTACGATATCCATCAATCATC
 ACTGAATCTTTTGTTTTCAAAGCAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA
 50 TCTCAGTGCTCTGTTGGCTGCCAGAGGCATTACTGCTCCAGAATCAAATTGAGCACTG
 TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT
 AACCAGGTCCCTTTGGCTTGGACACTCATGGGAAGTGACCTGGGTTTGATTATTTATCAT
 ATGCTCTAATACTTTACTCTGTCTGAAGCTGAACCTCTCCAGAAGCTGCATCCAAGGCCTT
 AAGTACCTGCACCTCCACCTCATCTTAATCCTTTCTTCTACACAGTCATCATTTGTGATTT
 55 CCATTACTCGTAGTACAGGAATGAGAGTTCCTTATTCCAGTTCTACTTAATGTGCTACA

CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAAGCTCAGG
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

5 MLTLNKTDLIPASFILNGVPGLEDTQLWISFPFCSMYVVMVGNCGLLYLIHYEDALHKPMYY
FLAMLSFTDLVMCSSTIPKALCIFWFHLKDIFDECLVQMFFIHTFTGMESGVLMLMALDRYV
AICYPLRYSTILTNPVIAKVGATFLRGVLLIIPFTFLTKRLPYCRGNLPHTYCDHMSVAKLSCG
NVKVNAIYGLMVALLIGGFDILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF
10 FSFFSHRFGHEIIPPSCHIIIVANIYLLLPPTMNPVYGVKTKQIRDCVIRILSGSKDTSYSYM (SEQ
ID NO: 259)

ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCAG
GACTGGAAGACACAACTCTGGATTTCCTTCCCATTCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCCTCTACCTCATTCACTATGAGGATGCCCTGCACAAACCCATG
15 TACTACTTCTTGGCCATGCTTTCTTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTTGATGAATGCCTTGTCCAG
ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGTATGCTTATGGCCCTGG
ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT
GCAAAGGTTGGGACTGCCACCTTCTGAGAGGGGTATTACTCATTATCCCTTTACTTTCTCT
20 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG
TCTGTAGCCCAAATTGTCCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
CCCTCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG
GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAGGCCTTTAATACCTGCACTGCCC
ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTCTTTTCCCACCGCTTTG
25 GGGAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA
CCCACTATGAACCCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCATAA
GGATCCCTTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

30 MSSTLGHNMESPNHTDVPDSVFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVL
HKPVYVFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFMMESTVLLAM
AFDRYVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA
VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC
VILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLPPLNPNVYGVKTKQIRKRVVRVFQSGQ
35 GMGIKASE (SEQ ID NO: 261)

ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCTG
TCTTCTTCTCCTCTGGGCATCCCAGGTCTGGAACAATTTCAATTTGTGGCTCTCACTCCCTGTG
TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG
40 AACCAGTCTTGCACAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT
GCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTCATGCCTTCTGCATGATGGAGTCCACT
GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
CAATCCTCACTGACACCATCATTGCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT
45 GCTCATGCTCCCATGTCCCTTCCTTATTGGGCGTTTGAACCTCTGCCAAAGCCATGTGATCC
TACACACGTAAGTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA
ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGACTTGTGTTGCAATTGG
TCTCTCCTATGCCCTAAGTGACACAAGCTGTCTTCTCGCTCTCATCCCATGAAGCTCGGTCCA
AGGCCCTAGGGACCTGTGGTTCCTATGTCTGTGTCATCCTCATCTCTTATACACCAGCCCTC
50 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTTGGC
CAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAAC
AGATCCGTAAAAGAGTTGTGAGGGTGTTCAAAAGTGGGCAGGGAATGGGCATCAAGGCAT
CTGAGTGA (SEQ ID NO: 262)

55

AOLFR143 sequences:

MLGLNGTPFQPATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMMYYFL
 SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACLVQMFFIHTFSFMESGILLAMSLDRFVAICY
 PLRYVTVLTHNRILAMGLGILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
 5 HVNNIYGLLVIIIFTYGMDSTFILLSYALILRAMLVISQEQLKALNTCMSHICAVLAFYVPIAVS
 MIHRFWKSAPPVVHVMMSNVYLFVPPMLNPIIYSVKTKERKILKFFHKSQA (SEQ ID NO:
 263)

ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAACACTCCAGCTGACAGGCATTCTCTG
 10 GGATACAAACAGGCCTCACCTGGGTGCCCCTGATTTTCTGCATCCTCTACATGATCTCCATT
 GTAGGTAACCTCAGCATTCTCACTCTGGTGTGTTTGGGAGCCTGCTCTGCATCAGCCCATGT
 ACTACTTCCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCTTTTCTACACTTCCCCT
 GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCCTGGTCCAGAT
 GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
 15 GCTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCACCACTCTCTTCCCTTTCCCTTTGTGGT
 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTCATCACTCCTACTGTCTCCATCCAGAT
 CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA
 TTTTACCTATGGTATGGACTCAACTTTTCATCCTGCTTTCCTACGCATTGATCCTGAGAGCC
 20 ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTACACA
 TCTGTGCAGTGTGGCCTTTTATGTGCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG
 AAAAGTGCTCCACCTGTTGTTTCATGTCTGATGTCCAATGTCTACCTGTTTGTACCAACCAT
 GCTCAACCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC
 TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

25

AOLFR144 sequences:

MGLFNVTHPAFFLLTGIPGLESSHWSLGPLCVMYAVALGGNTVILQAVRVEPSLHEPMMYYFL
 SMLSFDVAISMATLPTVLRFTCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD
 PLRYATVLTTEVIAAMGLGAAARSFITLPLPFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI
 30 NSIYGLFVLVSTFGMDLFFIFLSYVILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
 TVHRFGKHVPCYIHLVMSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

ATGGGGTTGTTCAATGTCACTCACCTGCATTCTTCTCCTGACTGGTATCCCTGGTCTGGA
 GAGCTCTCACTCCTGGCTGTCAGGGCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
 35 AATACAGTGATCCTGCAGGCTGTGCGAGTGGAGCCCAGCCTCCATGAGCCCATGTACTACT
 TCCTGTCCATGTTGTCCTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC
 CGAACCTTCTGCCTCAATGCCCGCAACATCACTTTTGATGCCTGTCTAATTCAGATGTTTCT
 TATTCACTTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG
 TGGCCATTTGTGACCCCTTGCGCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT
 40 GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCTTTTCCCTCTTCCCTTTCTTATTAAGA
 GGCTGCCTATCTGCAGATCCAATGTTCTTTCTCACTCCTACTGCCTGCACCCAGACATGATG
 AGGCTTGCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTGTCTTGTATCCAC
 CTTTGGCATGGACCTGTTTTTATCTTCTCCTATGTGCTCATTCTGCGTTCTGTCATGG
 CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTACATATCCTGGC
 45 TGTAATGCAATTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT
 GTCCCATGCTACATACATGTCTCATGTCAAATGTGTACCTATTTGTGCTCCTGTGCTCAA
 CCTCTCATTTATAGCGCAAGACAAAGGAAATCCGCCGAGCCATTTTCCGCATGTTTCAC
 CATACAAAATATGA (SEQ ID NO: 266)

AOLFR145 sequences:

MSVQYSLSPQFMILLSNITQFSPIFYLTSPFGLGKHWIFPFFFMVMVAISGNCFILIIKTNPRLH
 TPMYYLLSLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESSVLLMMSFD
 RFVAICHPLRYSVIITGQQVVRAGLIVFRGPVATIPVLLLKAFPYCGSVVLSHSFCLHQEVIQLA
 5 CTDTTFNLYGLMVVFTVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVF
 FVPMGLSLVHRFGKHAPPAIHLMLANVYLFVPPMLNPIIYSIKTKEIHRAIKLLGLKKASK
 (SEQ ID NO: 267)

ATGTCAGTCCAATATTCGCTCAGTCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG
 10 CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTTCATCC
 CCTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG
 ACCAACCCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT
 GGGGCTGTGTGTGTCCACGTTGCCACCACCTATGGGGATCTTCTGGTTAACTCCAGAGT
 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCTTCATGGAGTC
 15 CTCAGTGCTCCTCATGATGTCCTTTGACCGCTTTGTGGCCATCTGCCACCCTCTGAGGTATT
 CGGTCATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC
 TGTGGCCACTATCCCTATTGTCCTCCTCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC
 TCTCCCACTCATTTTGCCTGCACCAGGAAGTGATACAGCTGGCCTGCACAGATACCACCTT
 CAATAATCTGTATGGACTGATGGTGGTAGTTTTCACTGTGATGCTGGACCTGGTGCTCATC
 20 GCACTGTCCTATGGACTCATCCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
 GCCGTGCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGCCCATG
 ATGGGGCTGTCCCTGGTGCACCGTTTTGGGAAGCATGCCCCACCTGCTATTCACTTCTTAT
 GGCCAATGTCTACCTTTTGTGCCTCCCATGCTTAACCCAATCATATACAGCATTAAAGACC
 AAGGAGATCCACCGTGCCATTATCAAACCTCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
 25 ID NO: 268)

AOLFR146 sequences:

MSQVTNTTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMVFLFLSM
 LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFMSFMESSVLLAMSVDCYVAICCP
 30 LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVCADIRLN
 SWYGFALALLIIVDPLLVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYIPMVGVSMT
 HRFKHA SPLVHVIMANIYLLAPPVMNPIIYSVKNKQIQWGMNLNLSLKNMHSR (SEQ ID NO:
 269)

ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
 35 GATTTGAGGCCTCCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC
 ATGGGCAATACCACCATCCTCACTGTCAATCGCACAGAGCCATCTGTCCACCAGCGCATGT
 ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCTCACCACTACCCACA
 GTCATGCAGCTTCTCTGGTTCAACGTTCTGATAGATCAGCTCTGAGGCCTGTTTGTCTAGTT
 40 TTTCTTCTTCATGGATTCTCCTTTATGGAGTCTTCTGTCTCCTGGCTATGTCCGTTGACT
 GCTATGTGGCCATCTGCTGTCCCTCCATTATGCCTCCATCCTCACCATGAAGTCATTGGT
 AGAACTGGGTTAGCCATCATTTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT
 CAAGCGACTGCCTTTCTGCCACTCCCACCTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA
 TGATCCGCCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGCTCTTGCTT
 45 GCTCATTATTATCGTGGATCCTCTGCTCATTTGTGATCTCCTATACACTTATTCTGAAAAATA
 TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCACAT
 TCTAGCTGTCTGCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA
 AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT
 GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTTAAATTTCT
 50 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

MPSASAMIIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYTVAVVGNCLLYLIVVEHSLHEPMF
 FFLSMLAMTDLILSTAGVPKALSIFWLGAAREITFPGLTQMFFLHYNFVLDLSAILMAMAFDHYV
 55 AICSPRLRYTTLTPKTIKSAMGISFRSFCILPDVFLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI
 NFWYGFVCPIMTVISDVILIAVSIAHLCAVFGPLSQDACQKALGTCGSHVCVILMFYTPAFFSI

LAHRFGHNVSRTFHMIFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO: 271)

5 ATGCCATCTGCCTCTGCCATGATCATTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCAT
TCTGGTAGGGATCCCAGGCCTGGAGCAATCCATGTGTGGATTGGAATTCCTTCTGTATC
ATCTACATTGTAGCTGTTGTGGGAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA
GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC
ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTGGCTAGGGGCTCGCGAAATCACATTCC
CAGGATGCCTTACACAAATGTTCTTCTTCACTATAACTTTGTCCTGGATTGAGCCATTCTG
10 ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATACCACCATCTT
GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTCGAAGCTTCTGCATCATC
CTGCCAGATGTATTCTTGCTGACATGCCTGCCTTCTGTCAGGACACGCATCATACCCACA
CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG
GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCCT
15 ACGCACACATCCTCTGTGCTGTCTTTGGCCTTCCCTCCCAAGATGCCTGGCAGAAAGCCCT
CGGCACITGTGGTTCTCATGTCTGTGTCATCCTCATGTTTATACACCTGCCTTTTCTCCA
TCCTCGCCCATCGCTTTGGACACAATGTCTCTCGCACCTTCCACATCATGTTTGCCAATCTC
TACATTGTTATCCACCTGCACTCAACCCCATGGTTTACGGAGTGAAGACCAAGCAGATCA
GAGATAAGGTTATACTTTTGTCTTCTAAGGTTACAGGATGA (SEQ ID NO: 272)

20

AOLFR148 sequences:

MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMYFLC
MLAGADIVLSTCTIPQALAIWFWRAGDISLDRCTQLFFIHSFISESGILLVMAFDHYLAICYPLR
YTTILTALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIPHTFCEHIGLAKYACNDIRINIWYG
25 FSILMSTVVLVDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCHILFYGSGIFTILTQRFGR
HIPPCIHPLANVCILAPPMLNPIYGIKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
GCCTACAGGACCAGCACATGTGGATTTCTATCCCATTCCTTCATTTCCTATGTCACCGCCCTT
30 CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT
ACCTCTTCTCTGCATGCTGGCTGGAGCAGACATTGTCCTCTCCACGTGCACCATTCCTCAG
GCCTTAGCTATCTTCTGGTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT
CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC
ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCCTACAAATGCTCTGATCAA
35 GAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT
TAAAAAGATTGACTTTCTGCCAGAATAATATTATCCACACACCTTTTGTGAACACATTGG
CCTAGCCAAATATGCATGTAATGACATTGCAATAAACATTTGGTATGGGTTTTCATTCTA
ATGTCGACGGTGGTCTTAGATGTTGTAATAATTTTATTTCTATATGCTGATTCTCCATGC
TGTCTTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTTGGCTCCCATG
40 TCTGCATCATCATCCTCTTTTATGGGTCTGGCATCTTACAATCCTTACCCAGAGGTTTGG
CGCCACATTCCACCTTGATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTTATTTATGGGATCAAAACCAAGCAAATCCAGGAACAGGTGGTTTCAGTTT
TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

AOLFR149 sequences:

MSNASLLTAFILMGLPHAPALDAPLFGVFLVYVLTVLGNLLILLVIRVDSHLHTTMYFLTNL
SFIDMWESTVTVPKLLMTLVFPSGRAISFHSCMAQLYFFHFLGGTECFLYRVMSCDRYLAISSYP
LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWQHLYLCDAPILKLACADTS
AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEGHRAFTQCASHCTVVLCTFFGPGFLFIYLR
50 PGSRKAVDGVAVFYTVLTPLLNPVVYTLRNKEVKALLKLKDKVAHSQSK (SEQ ID NO:
275)

ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC
TGGACGCCCCCTCTTTGGAGTCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
55 CCTCATCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCTCA
CCAACCTGTCGTTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC

TTTGGTGTTCCTCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTCT
 TTTACTTCTAGGGGGCACCAGTGTTCCTCTACAGGGTCATGTCCTGTGATCGCTACCT
 GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG
 GCCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACTTTCC
 5 ATTTGCCCTACTGTGGACCCAAGTGGATCCAGCACTATTTGTGTGATGCACCGCCCATCCT
 GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTTGTGACTGTTGGAATA
 GTGGCCTCGGGCTGCTTTGTCCTGATAGTGTCTGCTATGTGTCCATCGTCTGTTCCATCCT
 GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
 GTGGTCCTTTGCTTCTTTGGCCCTGGTCTTTTCATTTACCTGAGGCCAGGCTCCAGGAAAGC
 10 TGTGGATGGAGTTGTGGCCGTTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGT
 ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC
 ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

AOLFR150 sequences:

15 MELGNVTRVKEFIFLGLTQSQDQSLVFLFLCLVYMTTLLGNLLIMVTVTCESRLHTPMYFLLR
 NLAIDLICFSSTTAPKVLLDLLSKKKTISYTSCMTQIFLHLLGGADIFSLSVMAFDCYMAISKPL
 HYVTIMSRGQCTALISASWMGGFVHSIVQISLLPLPFCGPNVLDTFYCDVPQVLKLTCTDTFA
 LEFLMISNGLVTTLWFIFLLVSYTVLMTLRSQAGGGRRKAISTCTSPHHCGRPACALHLCLC
 PALHCPPHRKGHLCHLHCHLPSAEPFDLHSEBPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

20 ATGGAGTTGGGAAATGTCACCAGAGTAAAGAATTTATATTTCTGGGACTTACTCAATCCC
 AAGACCAGAGTTTGGTCTTGTTCCTTTTATGTCCTGTGTACATGACGACTCTGCTGGGA
 AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTACACCCCCATGTAATCCT
 GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAAGTCTCTAAAGTCTTGC
 25 TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT
 CTTCCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTGTGATGGCGTTTACTGCTACA
 TGGCCATCTCCAAGCCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
 CATCTCTGCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC
 CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCTCT
 30 AAACCTACTTGCACCTGACACTTTTGCTCTTGAGTTCTTGATGATTTCACCAATAGGCCTGGT
 CACTACCCTGTGGTTTATCTTCCTGCTTGTGTCTACACAGTCATCCTAATGACGCTGAGGT
 CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGACCTCCCCACATCACTGTG
 GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCAC
 AGAAAAGGCCATCTCTGTACCTTCACTGTCTCTCCCTCTGCTGAACCCTTTGATCTACA
 35 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
 CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

40 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYILITLAGNLCMILLIRTNSHLQTPMYFFLGHL
 FVDICYSSNVTPNMLHNFLSEQKTISYAGCFTQCLLFIALVITEFYILASMLDRYVAICSPLHYS
 SRMSKNICVCLVTIPYMYGFLSGFSQSLLTFHLSFCGSLEINHFYCADPPLIMLACSDTRVVKMA
 MFVAVAGFNLSSSLFIILLSYLFIFAAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTLCMYVRPSE
 KSVBESKITA VFYTFLSPLMLNPLIYSLRNTDVLAMQMQMIRGKSFHKIAV (SEQ ID NO: 279)

45 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC
 CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCCTTGCGATCTACCTAATCACACTGGCAGG
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATTCCACCTGCAAAACACCATGTAATTC
 TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT
 GCACAAATTCCTCTCAGAACAGAAGACCATCTCCTACGCTGGATGCTTACACAGTGTCTT
 50 CTCTTCATCGCCCTGGTGATCACTGAGTTTACATCCTTGCTTCAATGGCATTGGATCGCTA
 TGTAGCCATTTGCAGCCCTTTGCATTACAGTTCAGGATGTCCAAGAACATCTGTGTCTGT
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT
 TCACTTATCCTTCTGTGGCTCCCTTGAATCAATCATTTCTACTGCGCTGATCCTCCTCTTA
 TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT
 55 TAATCTCTCAAGCTCTCTCTTCATCATTCTCTGTCTATCTTTTCATTTTGCAGCGATCTT
 CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTCTACGTGTGCTTCCACCTGACA

ATAGTCACTTTGTTTTATGGAACCTCTTCTGCATGTACGTAAGGCCTCCATCAGAGAAGT
CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTTGAGCCCAATGCTGAACCC
ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA
AAATCCTTTCATAAAATTGCAGTTTAG (SEQ ID NO: 280)

5

AOLFR152 sequences:

MDQINHTNVKEFFLELTRSRELEFFLVVFFAVYVATVLGNALIVVTITCESRLHTPMYFLLRN
KSVLDIVFSSITVPKFLVDLLSDRKTISYNDCMAQIFFHFAGGADIFFLSVMAYDRYLAIKPL
HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT
10 FALELFMISNGLVTLWFLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVTLHFVPCV
YIYCRPFMTLPMDTTISNNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLGPSESARKWG (SEQ ID
NO: 281)

ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCCTGGAACCTTACACGTTCCC
15 GAGAGCTGGAGTTTTTCTTGTGTTTGGTCTTCTTTGCTGTGTATGTAGCAACAGTCCCTGGG
AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCTACACACTCCTATGTAATTC
TCCTGCGGAACAAATCAGTCCTGGACATCGTTTTTTCATCTATCACCGTCCCCAAGTTCCTG
GTGGATCTTTTATCAGACAGGAAAACCATCTCTACAATGACTGCATGGCACAGATCTTTT
TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC
20 CTTGCAATCGCCAAGCCCCTGCATATGTGACCATGATGAGGAAAGAGGTGCGGTGGCC
TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCAATCAATCATCCAGGTAATTCTGATGC
TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG
GTAAAACTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC
TGGTGACCCTGCTCTGGTTCTCCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG
25 AGATCCCCTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCACATGCTG
GTGGTGACTCTTCACTTCGTGCCTTGTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC
CATGGACACAACCATATCCATTAATAACACGGTCATTACCCCCATGCTGAACCCCATCATC
TATTCCTTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG
CCTTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)

30

AOLFR153 sequences:

MSKTSLVTAFLTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTPKMLMTLVSPSGRAISFHSQVAVLYFFHFLGSTECFLYTVMSYDRYLAIKYPL
RYTSMMSGSRCALLATSTWLSGSLHSAVQTLTFHLPYCGPNQIQHYLCDAPPILKLACADTSA
35 NEMVIFVDIGLVASGCFLLIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVLCTFFVXCVFIYLR
PGSRDVVDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLKRDKVAHSQGE (SEQ ID NO:
283)

ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
40 TGGACGCCCCACTCTTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTT
TCCACTTCCTGGGGAGCACCAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACTTG
45 GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG
CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTATTGTGTGATGCACCGCCCATCCTGA
AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGCTAGT
GGCCTCGGGCTGCTTTCTCCTGATAGTGCTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC
50 GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT
GGTCCTTTGCTTTTTGTNNCCTGTGTTTTCAATTACCTGAGACCAGGCTCCAGGGACGTCG
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCCTGTTGTGTAC
ACCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT
TCTCAGGGAGAATAA (SEQ ID NO: 284)

55

AOLFR156 sequences:

MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFYTFIHDNLLIFS AVR
 DTHLGNPMYNFISIFSFLEIWYTTATIPKMLSNLISEKKAISMTGCILQMYFFHSLNSEGILLTT
 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGLLILLPEIVMISTLPFCGPNQIHQIFCDLVP
 5 VLSLACTDTSMLIEDVIHAVTIIITFLIHALSYVRIVTVILRIPSEGRQKAXSTCAGHLMVFLIFFG
 SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPIIYSLRNKDMNNAIKKLFCLQKVLNKPFG
 (SEQ ID NO: 285)

ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
 10 ACCAATCAACAGTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
 CCTGTACTTCTTTCTTTACTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT
 CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT
 CCTTTCTGGAGATCTGGTACACCACAGCCACCATTCCCAAGATGCTCTCCAACCTCATCAG
 TGAAAAGAAGGCCATCTCAATGACTGGCTGCATCTTGCAAGATGTATTCTTCCACTCACTT
 15 GAAAACTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA
 ACCCTCTTCGCTATCAAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTCC
 TGCCTCTTCGGTTTCCTTATCCTGCTTCCCGAGATTGTGATGATTTCACACTGCCTTTCTG
 TGGGCCCCAACAAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT
 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTGCTGTGACCATCATTAACCT
 20 TCCTAATCATTGCCCTGTCTATGTAAGAATTGTCAGTGTGATATTGAGGATTCCCTCTTCT
 GAAGGGAGGCAAAAGGCTNTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGATATTCT
 TTGGCAGTGTATCACTCATGTACTTGCGTTTCAGCAACACTTATCCACCAGTTTGGACAC
 AGCCATTGCACTGATGTTTACTGTACTTGCTCCATTCTCAATCCCATCATTTATAGCCTGA
 GAAACAAGGACATGAACAATGCAATTAATAAACTGTTCTGTCTTCAAAAAGTGTGAACA
 25 AGCCTGGAGGTAA (SEQ ID NO: 286)

AOLFR157 sequences:

MAMDNVTA VFQFLIGISNYPQWRDFTFFTLVLIYSLTLLGNGFMIFLIHFDPNLHTPIYFFLSNL
 SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP
 30 LRYSVVMNGPVCVCLVATSWGTSVL TAMLILSLRLHFCGANVINHFACEILSLIKLTCSDTSL
 NEFMILITSIFTL LPPGFVLLSYRIAMAIIRISLQGR LKAFTTCGSHLTVVTIFYGSAISM YMKT
 QSKSSPDQDKFISVFY GALT PMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTCACAGCAGTGTTTCAGTTTCTCCTTATTGGCATTCTAACTATCC
 35 TCAATGGAGAGACACGTTTTTACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
 AATGGATTATGATCTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
 CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
 TGCATTGTTTCTTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTC
 TCCTTGGCTTTGGCCACAGCAGAGTGCTCTCTACTGGCTGCCATGGCCTATGACCGTGTGG
 40 TTGCTATCAGCAATCCCCTGCGTTATTAGTGTTATGAATGGCCAGTGTGTGTCTGCTT
 GGTGCTACCTCATGGGGGACATCACTTGCTCACTGCCATGCTCATCCTATCCCTGAGG
 CTTCACTTCTGTGGGGCTAATGTCATCAACCATTTTGCCTGTGAGATTCTCTCCCTCATTA
 GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTACCC
 TGCTGCTACCATTTGGGTTTGTCTCCTCTCCTACATACGAATTGCTATGGCTATCATAAGG
 45 ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG
 TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAAACCTCAGTCCAAGTCTCCCC
 TGACCAGGACAAGTTTATCTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCTG
 ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG
 ACATGA (SEQ ID NO: 288)

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AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPIFLFSLMYLATMLGNLLIILAVNSDSLHTPMYFLLSI
 LSLVDICFTSTTMPKMLVNIQAQAQSINYTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP
 LRYNVIMNPKLCGLLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFCELAHILKLACSDVLIN
 55 NILVYLVTSLGVPVPLSGHFSYTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSLFYGTGFGVYLS
 GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKDM LKALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTGACGGGGATC
 CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCCGTGCCATGTACCTGGCCACAATGCTGGG
 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCACCTCCACACCCCCATGTACTTCC
 5 TCCTCTCTATCCTGTCCTTGGTCGACATCTGTTTCACCTCCACCACGATGCCCAAGATGCTG
 GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTACCCAAATCTGCT
 TTGTCCTGGTTTTTTGTTGGATTGGAAAATGGAATTCTGGTCATGATGGCCTATGATCGATT
 TGTGGCCATCTGTCACCCACTGAGGTACAATGTCATCATGAACCCCAAACTCTGTGGGCTG
 CTGCTTCTGCTGTCCTTCATCGTTAGTGTCTGGATGCTCTGCTGCACACGTTGATGGTGCT
 10 ACAGCTGACCTTCTGCATAGACCTGGAAATCCCCACTTTTTCTGTGAAGTAGCTCATATTC
 TCAAGCTCGCTGTTCTGATGTCCTCATCAATAACATCCTGGTGTATTTGGTGACCAGCCT
 GTTAGGTGTTGTTCCCTCTCTGCGGATCATTITCTCTTACACACGAATTGTCTCCTCTGTCA
 TGAAAATTCCATCAGCTGGTGGAAAGTATAAAGCTTTTTCCATCTGCGGGTCACATTTAAT
 CGTTGTTTCCCTGTTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT
 15 CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC
 ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG
 GATACCATCTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

20 MGPRNQTA VSEFLMKVTEDEPELKLIPFSLFLSMYLVTLGNLLILLA VISDSHLHTPMYFLLFN
 LSFTDICLTTTTVPKILVNIQAQNSITYTGCLTQICLVLFAGLESCFLAVMAYDRYVAICHPL
 RYTVLMNVHFWGLLILLSMFMTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDTL
 INNILYFASSVFGAIPLSGIIFSYSQIVTSVLRMPARSARGKYKAFSTCGCHLSVFSLFYGTAFGVYIS
 SAVAESSRITAVASVMYTVVPQMMNPFYSLRNKEMKKALRKLIGRLFPF (SEQ ID NO: 291)

25 ATGGGACCCAGAAACCAACAGCTGTTTCAGAATTCTTCTCATGAAAGTGACAGAGGAC
 CCAGAACTGAAGTTAATCCCTTTTCAGCCTGTTCCGTGCCATGTACCTGGTCACCATCCTGG
 GGAACCTGCTCATTTCTCCTGGCTGTCATCTCTGACTCCACCTCCACACCCCCATGTACTTC
 CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAACCACAACCACAGTCCCAAGATCCT
 30 AGTGAACATCCAAGCTCAGAATCAGAGTACACTTACACAGGCTGCCTCACCAGATCTGT
 CTTGTCTTGGTTTTTGTGCTGGCTTGGAAAGTTGCTTCTTGCAGTCATGGCCTACGACCGCTA
 TGTGGCCATTGTCACCCACTGAGGTACACAGTCCTCATGAATGTCCATTTCTGGGGCTTG
 CTGATCTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT
 GCAGCTGTCCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTTCAGGTC
 35 ATCAAGCTCGCCTGTTCTGACACCCTCATCAACAACATCCTCATATATTTTGCAAGTAGTGT
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTCTCAAATAGTCACCTCTGTTT
 TGAGAATTGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTCACCTCTC
 TGTTTTTCTTCTTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTGTGCTGAGT
 CTTCCCGAATTACTGCTGTGGCTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
 40 CTTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAACTTATTGGTAG
 GCTGTTTCTTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

45 MPMQLLLTDFIIFSIRFIINSMEARNQTAISKFLLGLIEDPELQPVLFSLFLSMYLVTLGNLLILL
 AVISDSHLHTPMYFFLSNLSFLDICLSTTTIPKMLVNIQAQNSITYSGCLTQICFVLFAGLENC
 LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLILLSLLTSVNNALLLSLMVLRSLFCTDLEIPLFF
 CELAQVIQLTCSDTLINNILIYFAACIFGGVPLSGHLSYQTITSCVLRMPASGKHKA VSTCGSHL
 SIVLLFYGAGLGVISSVVTDSRPRTAVASVMYSVFPQMVNPFYSLRNKDMKGTLRKFIGRIP
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

50 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG
 CATGGAAGCGAGAAACCAACAGCTATTTCAAAATTCCTTCTCCTGGGACTGATAGAGGAT
 CCGGAACTGCAGCCCGTCTTTTCAGCCTGTTCCGTGCCATGTACTGGTACCATCCTGGG
 GAACCTGCTCATCCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCCATGTACTTCT
 55 TCCTCTCCAATCTCTCCTTTTGGACATTTGTTTAAGCACAACCACGATCCCAAGATGCTG
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCAGATCTGCT

TTGTCCTGTTTTTGTCTGGCTTGGAAAAATTGTCTCCTTGCAGCAATGGCCTATGACCGCTAT
 GTGGCCATTTGTACCCCCCTTAGATACACAGTCATCATGAACCCCCGCTCTGTGGCCTGC
 TGATTCTTCTCTCTCTGTTGACTAGTGTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTG
 AGGCTGTCCTTCTGCACAGACCTGGAAATCCCGCTCTTCTTCTGTGAATGGCTCAGGTCA
 5 TCCAACTCACCTGTTTCAGACACCCTCATCAATAACATCCTGATATATTTTGCAGCTTGATA
 TTTGGTGGTGTTCCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT
 GAGAATGCCATCAGCAAGTGGAAAGCACAAAGCAGTTTCCACCTGTGGGTCTCACCTCTCC
 ATTGTTCTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC
 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTCCCTCAAATGGTGAACCCC
 10 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG
 ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTTCAGGTTTCTAGAGTAA (SEQ ID
 NO: 294)

AOLFR161 sequences:

15 MEPRNQTSA SQFILLGLSEKPEQETLLFSLFFCMYLV MVVGNLLIILAISIDSHLHTPMYFFLANL
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCLIQMYFFHFFGIVDSVIIAMMAYDRFVAICHPLH
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
 IFILIVAGMVIATPFVCILASYARILVAIMKVPSAGGRKKAFTSCSSHLSVVALFYGTTIGVYLCF
 SSVLTTVKEKASAVMYTAVTPMLNPFYISLRNRDLKGALRKL VNRKITSSS (SEQ ID NO: 295)

20 ATGGAACCAAGAAACCAAAACCAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC
 CAGAGCAGGAGACGCTTCTCTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG
 GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCACCTCCACACCCCCATGTACTTCT
 TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT
 25 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC
 TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGT
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTCGCCTG
 CTGGTCGGCGCCCTCTGGGCGTTTTCTGCTTCATCTCACTCACTCACATCCTCCTGATGGC
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC
 30 TCCGACTTTCGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT
 GGTGATAGCCACGCCCTTTGTCTGCATCCTAGGCTCCTATGCTCGCATCCTTGTGGCCATCA
 TGAAGTGCCCTCTGCAAGGCGGCAGGAAGCCCTTCTCCACCTGCAGCTCCCACTGTC
 TGTGGTTGCTCTCTTCTATGGGACCACCATTTGGCGTCTATCTGTGTCCCTCCTCGGTCTCA
 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCCATGCTGAATCC
 35 CTTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG
 AAAGATCACCTCATCTTCCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

40 MMRLMKEVRGRNQTEVTEFLLGLSDNPD LQGVLFALFLLIYMANMVG NLMIVLIKIDLCLH
 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA
 YDRYAAIWNPLLYPVLVSGRICFLLIATSF LAGCGNAAIHTGMTFRLSFCGSNRINHFYCDTPPL
 LKLSCSDDTHFNIGIVIMAFSSFVISCVMIVLSYLCIFIAVLKMP SLEGRHKAFSTCASYLMAVTIF
 FGITLFMYLRPTSSYSMEQDKVVS VFYTVIIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
 NO: 297)

45 ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAAGTAACAGAATTTCTC
 CTCTTAGGACTTTCCGACAAATCCAGATCTACAAGGAGTCCTCTTTGCATTGTTTCTGTTGAT
 CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAAGATTGATCTCTGT
 CTCCACACCCCCATGATTTCTTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT
 50 TCCGTCACTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG
 GATGTGCTGCCCAGTTCTACTTCTTTGGCTCCTTCTGGGGACTGAGTGCTTCTGTTGGCC
 ATGATGGCATATGACCGCTATGCAGCCATTTGGAACCCCCTGCTCTACCCAGTTCTCGTGT
 CTGGGAGAATTTGCTTTTGTCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC
 CATACATACAGGGATGACTTTTAGGTTGTCTTTTGTGGTTCTAATAGGATCAACCATTTCT
 55 ACTGTGACACCCCGCCACTGCTCAAACCTCTTGTCTGTATACCCACTTCAATGGCATTGTG
 ATCATGGCATTCTCAAGTTTTATTGTCATCAGCTGTGTTATGATTGTCCTCATTTCCTACCT

GTGTATCTTCATTGCCGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC
 ACCTGTGCCCTCTTACCTCATGGCTGTCACCATATTCTTTGGAACAATCCTCTTCATGTACTT
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA
 ATAATCCCTGTGCTAAATCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC
 5 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYSLTVVGNSTLIVLICNDSCLHTPMYFFTG
 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
 10 LYAQAMSIKLCALLVAVSYCGGFINSSHTKTFNFNCRENIIDDFCDLLPLVELACGEKGGYK
 IMMYFLLASNVICPAVLILASYLFIITSVLRISSSKGYLKAFSTCSSHLTSVTLYYGSILYIYALPRS
 SYSFDMDKIVSTFYTVVFPMLNLMYSLRNKDVKEALKKLLP (SEQ ID NO: 299)

ATGCAGAGGAGCAATCATACAGTGACTGAGTTTATACTGCTGGGCTTCACCACAGACCCA
 15 GGAATGCAGCTGGGCCTCTTCGTGGTGTCTCTGGGCGTGACTCTCTCACTGTGGTAGGAA
 ATAGCACCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC
 ACTGGAAATCTGTCTGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCACTTCTTCTTCT
 CTGCAGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
 20 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTCAATCATCACCAAGAAAAACGTTTTC
 CTTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTGTCTCCCTGGTGG
 AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCTGCTGGCCTCCAA
 TGTCATCTGCCCCGAGTGCTCATCCTGGCCTCCTACCTCTTTATCATCACCAGTGTCTTGA
 25 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCACCTGACCTCT
 GTCACITTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT
 TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG
 ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAATTCTCCCATAA (SEQ
 ID NO: 300)

30

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFSDYLELQIPLFFVFLAVYGFSVVGNLGMIVIIKINPKLHTPMYFFLN
 HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTELILFAVMAYDHFVAICNP
 LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHHFCELSLISLSPDSYL
 35 SQLLLFTVATFNEISTLLIILTSYAFIIVTLKMPASGHRKVFSTCASHLTATIFHGTLFLYCVP
 NSKNSRHTVKVASVFYTVVIPLNPLIYSLRNKDVKDAIRKIINTKYFIKHRHWYPNPFVIEQ
 (SEQ ID NO: 301)

ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACTCTCTTGGGCTTCTCAG
 40 ATTACCTGGAAGTCAAATTCCCCTCTTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG
 GTAGGGAATCTTGGGATGATAGTGATCATCAAAATTAACCCAAAATTGCATACCCCCATGT
 ATTTTTTCTCAACCACTCTCCTTTGTGGATTTCTGCTATTCTCCATCATTGCTCCCATGA
 TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT
 CTTTTTCTTTTGACCTTTGTAGTGACTGAATTAATTCTATTTGCGGTGATGGCCTATGACC
 45 ACTTTGTGGCCATTGCAATCCTCTGCTCTACACAGTTGCCATCTCCCAGAACTCTGTGCC
 ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG
 CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTCTTCTGTGAGTTATCCTCC
 CTGATATCACTCTCTTACCTGACTCTTATCTCAGCCAGTTGCTTCTTTCACTGTTGCCAC
 TTTTAAATGAGATAAGCACACTACTCATCTTCTGACATCTTATGCATTTCATATTGTACCA
 50 CCTTGAAGATGCCCTTCAGCCAGTGGGCAACGCAAAAGTCTTCTCCACCTGTGCCCTCCACCT
 GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA
 ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCCTGTGTGA
 TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
 AAAAAATATTTTCATATTAAACATAGGCATTGGTATCCATTTAATTTGTTATTGAACAATA
 55 A (SEQ ID NO: 302)

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
 SNLSFLDICVVSSTAPKMLSDIITEQKTISFVGCAQYFVFCGMGLTECFLLAAMAYDRYAAICN
 PLYTVLISHTLCLKMVVGAYVGGFLSSFIETYSVYQHDFCGPYMINHFFCDLPPVLALSCSDTF
 5 TSEVVTFIVSVVVGIVSVLVVLISYGYIVA AVVKISSATGRTKAFSTCASHLTAVTLFYGSGFFM
 YMRPSSSYSLNRDKVVSIFYALVIPVVPNTIYSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
 (SEQ ID NO: 303)

ATGGCTGTAGGAAGGAACAACACAATTGTGACAAAATTCATTCTCCTGGGACTTTTCAGACC
 10 ATCCTCAAATGAAGATTTTCCCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC
 TGGAACCTTAAGCCTCATTGCCCTCATTAGATGGACTCTCACCTGCACATGCCCATGTACT
 TCTTCTCAGTAACCTGTCCTTCTCGGACATCTGCTATGTGCTCCACCGCCCCCTAAGATG
 CTGTCTGACATCATCACAGAGCAGAAAACCATTTCCCTTTGTTGGCTGTGCCACTCAGTACT
 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG
 15 GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATACTTTGTTTAA
 AGATGGTGGTGGCGCCTATGTGGGTGGATTCCCTAGTTCTTTCAATTGAAACATACTCTGT
 CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTCTGTGACCTCCCTCCAG
 TCCCTGGCTCTGTCTGCTCTGATACCTTCACCAGCGAGGTGGTGACCTTCATAGTCAGTGTT
 GTCGTTGGAATAGTGTCTGTGCTAGTGGTCTCATCTCTTATGGTTACATTGTTGCTGCTGT
 20 TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTCTCACCTG
 ACTGCTGTGACCCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTTCAGCTA
 CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCCGTGGTGAAT
 CCCATCATCTACAGTTTATAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA
 AGGGACCCCGGGATTTCTACGGTGGACCATTCTTTTATGACCTTGGGCTAA (SEQ ID
 25 NO: 304)

AOLFR166 sequences:

MEMENCTRVKEFIFLGLTQNREVSLVLFLLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH
 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFQMFHLHIGGVDVFSLSVMALDRYVAISKPL
 30 HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLPLPFCGPNVLDTFYCDVHRVLKLAHTDIFIL
 ELLMISNNGLLTTLWFFLLVSYIVLSLPKSQLAGEGRRAISTCTSHITVTVLHFVPCIVYARP
 FTALPMDKAISVTFVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

ATGGAGATGGAAAACTGCACCAGGGTAAAAGAATTTATTTTCTTGGCCTGACCCAGAATC
 35 GGGAAGTGAGCTTAGTCTTATTTCTTTTCTACTCTTGGTGTATGTGACAACTTGTCTGGGA
 AACCTCATCATGGTCACTGTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTTT
 GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTTCCATCACAGTGCCCAAGGTTCTGG
 TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
 TTCCACCTTATTGGAGGGGTGGATGTATTTTCTCTTTCGGTGATGGCATTGGATCGATATG
 40 TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT
 CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGCAGATTCCCTGTTGCTC
 CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCTT
 CAACTGGCCCATACAGACATTTTCACTTGAACCTACTAATGATTTCCAACAATGGACTG
 CTCACCACACTGTGGTTTTTCTGCTCCTGGTGTCTACATAGTCATATTATCATTACCCAA
 45 GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACTGT
 GGTGACCCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCA
 TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTCAACCCCTTGATCTAC
 ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT
 TCTGATAGAAAATAG *SEQ ID NO: 306)

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AOLFR167 sequences:

MSITKAWNSSSVTMFILLGFTDHPQLQALLFVTFGLGIYLLTLAWNLAFLIRGDTHLHTPMYFF
 LSNLSFIDICYSSAVAPNMLTDFFWEQKTISFVGCAAQFFFFVGMGLSECLLTAMAYDRYAAI
 SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFCGPNINHFFCDLPPVLALSCSDT
 55 FLSQVVNFLVVVTVGGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTTLLFGTAL

FVYLRPSSSYLLGRDKVVSFVYSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID NO: 307)

5 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA
CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCCTGGGCATCTATCTTACCACC
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA
TGTAATCTTCTTAAGCAACTTATCTTTTATTGACATCTGCTACTCTTCTGCTGTGGCTCCC
AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTGTGGGCTGTGCTGCTC
AGTTTTTTTTCTTTGTGGCATGGGTCTGTCTGAGTGCCTCCTCCTGACTGCTATGGCATA
10 GACCGATATGCAGCCATCTCCAGCCCCCTTCTTACCCCACTATCATGACCCAGGGCCTCT
GTACACGCATGGTGGTGGGGCATATGTTGGTGGCTTCCTGAGCTCCCTGATCCAGGCCAG
CTCCATATTTAGGCTTCACTTTTGGGACCCCAACATCATCAACCACTTCTTCTGCGACCTCC
CACCAGTCCCTGGCTCTGTCTTGTCTGACACCTTCCTCAGTCAAGTGGTGAATTTCTCTCGT
GTGGTCACTGTGCGAGGAACATCGTTTCTCCAACCTCCTTATCTCCTATGGTTACATAGTGT
15 CTGCGGTCTCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCCT
CGCATCTGATGGTGGTGGTACTCTGCTGTTTGGGACAGCCCTTTTCGTGTACTTGGGACCCAG
CTCCAGCTACTTGTAGGCAGGGACAAGGTGGTGTCTGTTTCTATTTCATTGGTGATCCCC
ATGCTGAACCCTCTCATTTACAGTTTGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
GTGTTGGAAGGAAGAAAGTGTTCCTTAG (SEQ ID NO: 308)

20

AOLFR168 sequences:

MEKINNVTETIFWGLSQSPEIEKVCFFVVSFFYIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
DICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLVHFFGCTEIFILTVMAYDRYVAICKPLHYM
TIMNRETCKNMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCDVHPVLKLACTETIVG
25 VVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRPD
TTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO:
309)

30 ATGGAAAAATAAACAACGTAACCTGAATTCATTTCTGGGGTCTTTCTCAGAGCCCAGAGA
TTGAGAAAGTTTGTGTTTGTGGTGTTCCTTCTTCTACATAATCATTCTTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAGTCACCCATGTATTTCTTTCTCAG
CTTCTTGTCTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCTTATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAAATGGCCTATGATCGTTATGTGGCT
35 ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACCT
ACCTTTTGTGGACCCAATGAGATAGATCACTACTTTTGTGATGTTACCCCTGTGTTGAAA
CTTGCTGACAGAAACATACATTGTTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG
CTCTGGGGAGTTTTGTTATCTTGTAAATCTCTACAGCATCATCCTAGTTTCCCTGAGAAAG
40 CAGTCAGCAGAAGGCAGGCGCAAAGCCCTCTCCACCTGTGGCTCCACATTGCCATGGTGC
TTATCTTTTTCGGCCCCCTGTACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT
GAGAAATGCAGAAGTAAAGAAATGCAATGAAGAAACTGTGGGGCAGAAATGTTTTCTTGA
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

45

AOLFR169 sequences:

MMDNHSSATEFHLLGFPGSQGLHHILFAIFFFFYLVTLMGNTVIIVIVCVDKRLQSPMYFFLSHL
STLEILVTIIVPMMLWGLLFLGCRQYLSLHVSINFSCGTMEFALLGVMAVDRYVAVCNPLRY
NIIMNSSTCIWVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLLKLSCDNTLLTEFI
50 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRRKAFSTFASHFTCVVIGYGSCFLYVKPKQTQ
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCTGGGTCCCAAG
55 GACTACACCACATTCTTTTTGCTATATTCTTTTCTTCTATTTAGTGACATTAATGGGAAAC
ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCTCT
CAGCCACCTCTTACCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG

GGATTGCTCTTCCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCCTG
 TGGGACCATTGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT
 AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT
 CATGGGTGTTTGGATTTCTTTCTGAAATCTGGCCCATCTATGCCACATTTAGTTTACCTTC
 5 CGCAAATCAAATTCATTAGACCATTTTTACTGTGACCGAGGGCAATTGCTCAAACCTGTCCT
 GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT
 TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCCTC
 AGCCTCTGGCCGAGGAAAGCCTTCTCCACTTTTGCCTCCCACTTCACCTGTGTTGTGATTG
 GCTATGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACACAGGGAGTTGAGTACAA
 10 TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCCCTGAATCCTTTTACTCT
 TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT
 GAAAGATTAG (SEQ ID NO: 312)

AOLFR170 sequences:

15 MSFTSLPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVVPVSSVSSSMVLCLYLSVS
 ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIVMVI
 ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDDLPHKVTFTGCMVQFYFHFSLGSTSFLIL
 TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH
 FFDNEPLLQLSCSDTRLLEFWDFLMAITFVLSFLVTLISYGYIVTTVLRIPSASSCQKAFSTCG
 20 SHLTLVFIGYSSITFLYVRPGKAHSVQVRKVVALVTSVLTPFLNPFLTFCNQTVKTVLQGQMQ
 RLKGLCKAQ (SEQ ID NO: 313)

ATGTCTTTCACTTCTCTCATACCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT
 TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTTGCCTTT
 25 CTCTCTCTATTCTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTTCAATGGTTCTCTGTCTC
 TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTCTCTTGTCATGCAGGGCCCCATACTG
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCTCTTGGGCTTCTCCTCCTTTGG
 TGAGCTGCAGGCCCTTCTGTATGGCCCTTCTCATGCTTTATCTTCTCGCCTTCATGGGAA
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC
 30 CTGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCAGGATGCTCT
 CAGACCTGTTGGTCCCCACAAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC
 CACTTTTCCCTGGGGTCCACCTCCTTCTCATCTGACAGACATGGCCCTTGATCGCTTTGT
 GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG
 GCTGGGGCTGCCTGGGCAGCTCCTTTCTAGCCATGGTACCCACTGTCCTCTCCCGAGCTC
 35 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTCTCCTG
 CAGTTGTCATGCTCTGACACTCGCCTGTTGGAATTCTGGGACTTTCTGATGGCCTTGACCTT
 TGTCTCAGCTCCTTCTGGTGACCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC
 GGATCCCCCTCTGCCAGCAGCTGCCAGAAGGCTTCTCCACTTGCGGGTCTACCTCACACT
 GGTCTTATCGGCTACAGTAGTACCATTCTTCTGTATGTCAGGCCTGGCAAAGCTCACTCT
 40 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTCACCCCTTTCTCAATCCCT
 TTATCCTTACCTTCTGCAATCAGACAGTAAAACAGTGCTACAGGGGCAGATGCAGAGGCT
 GAAAGGCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

45 MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAISTAMSPKLMIDLCDKIAISLSACMGQLFI
 EHLLGGAEVFLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVMIGGFVHSVQIVFLYSLP
 ICGPNVIDHSVCDMYPLLELLCLDTYFIGLTVVANGGICMVIFTLLISCGVILNFKTYSQEER
 HKALPTCISHIIVVALVFVPCIFMYVRPVSNFPFDKLMTVFYSIITLMLNPLIYSLRQSEMKNAM
 KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

50 ATGGTGGGAAACCTCCTCATTTGGGTGACTACTATTGGCAGCCCCCTCTTGGGCTCCCTAA
 TGTACTTCTTCTTGCCTACTTGTCACTTATGGATGCCATATATCCACTGCCATGTCACCC
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCTTGTGAGCTTGCATGGGTC
 AGCTCTTCATAGAACTTACTTGGTGGTGCAGAGGCTTCTCTTTGGTGGTGATGGCCTA
 55 TGATCGCTATGTGGCTATCTTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT
 TGCATCCTTCTGTTGGTGGTGGCCATGATTGGAGGTTTGTGCACTCTGTGGTTCAAATTGT

CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
 ACCCATTTGTTGGAAGTGTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
 TGGTGGAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA
 ACTTCCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAAGCCCTGCCTACCTGCATCTCCCA
 5 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTTATGTATGTTAGACCCGTTTCCA
 ACTTTCCCTTTGATAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA
 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCACACTGAACATATTTATTCCTAGTTCTA
 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

10

AOLFR172 sequences:

MAETLQLNSTFLHPNFFILTGFPGLGSAQTWLTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM
 FLLLAILAATDLGLATSIAPGLLAVLWLGPRSPVYAVCLVQMFFVHALTAMESGVLLAMACDR
 AAAIGRPLHYPVLVTKACVGYAALALALKAVAVVPFLLVAKFEHFQAKTIGHTYCAHMAV
 15 VELVVGNTQATNLYGLALSLSAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSSHICVIL
 AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLPPLNPLIYGARTKQIRDRLLETFTFRKSPL
 (SEQ ID NO: 317)

ATGGCAGAACTCTACAACTCAATTCCACCTTCCTACACCCAACTTCTTCATACTGACTG
 20 GCTTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCCATTATCT
 GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTGCA
 CCAGCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT
 ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT
 GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
 25 CATGGCCTGTGATCGTGTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCCTGGTCACC
 AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
 CTTTCCCACTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA
 TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGTAACACACAGGCCACCAACTTATA
 TGGTCTGGCACTTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
 30 GGACTCATTGCCCATGCTGTGCTGCAGTCACTACCCGGGAGGCCCATGCCAAGGCCTTGT
 GTACATGTAGTTCTCACATCTGTGTCACTTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC
 CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT
 CTACTTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCCGCACCAAGCAGATC
 AGAGACCGACTCCTGGAAACCTTCACATTCAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

35

AOLFR173 sequences:

MSHTNVTIFHPAVFVLPPIGLEAYHIWLSIPLCLYTTAVLGNSILIVVIVMERNLHVPMPYFFLS
 MLAVMDILLSTTTPKALAIWLAHNIADFACVTQGGFVHMMFVGESAILLAMAFDRFVAIC
 APLRYTTVLTWPVVGRIALAVITRSFCIIFVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
 40 NIWYGFSPVIVMVIDVILIAVSYSILIRAVFRLPSQDARHKALSTCGSHLCVILMFYVPSFFTL
 THHFGRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREGVAHRFFDIKTWCCTSPGLS
 (SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCTCCTGGCATCCCTGG
 45 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTTGCCTCATTTACATCACTGCAGTCC
 TGGGAAACAGCATCCTGATAGTGTTATTGTGATGGAACGTAACCTTCATGTGCCCATGTA
 TTCTTCTCTCAATGCTGGCCGTCATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG
 CCTAGCCATCTTTTGGCTTCAAGCACATAACATTGCTTTTGTATGCCTGTGTACCCCAAGGC
 TTCTTTGTCCATATGATGTTTGTGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
 50 CTTTGTGGCCATTTGTGCCCCACTGAGATATAACAACAGTGCTAACATGGCCTGTTGTGGGG
 AGGATTGCTCTGGCCGTCATACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT
 GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCTCCTCACTCCTACTGTGAGCATATTGGA
 GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTTGGTATGGCTTCTCAGTGCCCAT
 TGTGATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG
 55 TGTTTCGTTTGGCCTCCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTGGCTCCACCT
 CTGTGTCATCCTTATGTTTTATGTTCCATCCTTCTTTACCTTATTGACCCATCATTTTGGGCG

TAATATTCCTCAACATGTCCATATCTTGCTGGCCAATCTTTATGTGGCAGTGCCACCAATGC
TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCACCGGTT
CTTTGACATCAAGACTTGGTGTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

5 **AOLFR175 sequences:**

MHFLSQNDLNLINLIPHLCLHRHSVIAGAFTHRHMKIFNSPSNSSTFTGFILLGFPCPREGQILLFV
LFTVVYLLTLMGNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKIISF
SGCFLQFYFFFSLGSTECFFLAVMAFDRLAICRPLRYPTIMTRRLCTNLVVNCWVLGFIWFLIPI
VNISQMSFCGSRIDHFLCDPAPLLTLTCKKGPVIELVFSVLSPLPVFMLFLFVGSYALVVRAVL
10 RVPSAAGRRAKAFSTCGSHLAVVSLFYGSVLVVMYGSPPSKNEAGKQKTVTLFYSVVTPLNPI
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGACCCG
TCATTACAGTAATTGCTGGTGCTTTTACAATTCACAGGCACATGAAAATCTTCAACAGCCCC
15 AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC
AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTACCTCCTGACCCTCATGGGCAATGGTTCC
ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA
ACTTCTCCTTCTTGGAGATATGTTATGTCACCTCCACAGTCCCCAGCATGCTGGCCAACCTC
CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCCTCCAGTTCTACTTTTCTTCTCC
20 TTGGGCTCTACAGAATGCTTTTCTGGCAGTTATGGCATTGATCGATACCTTGCCATCTG
TCGGCTCTACGCTATCCAACCATTATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT
GCTGGGTACTTGGTTTCATCTGGTCTTGTATTCCTATCGTCAACATCTCCCAAATGTCCTTC
TGTGGATCTAGGATTATTGACCACTTCCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG
CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTCTGTCTTAAGTCTCTGCCTGTCTTTATGC
25 TCTTTCTCTTCATTGTGGGGTCTATGCTCTGGTCTGTGAGAGCTGTGTTGAGGGTCCCTTCA
GCAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCCAACATCTAAGAATGAAGCTGGAAAGC
AGAAGACTGTGACTCTGTTTTATTCTGTTGTTACCCCACTGCTTAACCCTGTGATATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:
30 322)

AOLFR176 sequences:

MFFIHSLSVTSVFLTALGPQNRTMHFVTEFVLLGFHGGQREMQSCFFSFLVLYLLTLLGNGAIVC
AVKLDRLHTPMYILLGNFALEIWIYSSTVPNMLVNLSSEKTSISFGCFLQFYFFFSLGTTTECF
35 LSVMAFYDRYLAICRPLHYPSIMTGKFCILVCVCWVGGLFCYPVPIVLISQLPFCGPNIDHLVCD
PGPLFALACISAPSTELICYTFNSMIFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV
VSLFYGTLMVMYVSPTSNGNPAGMQKIITLVYTAMTPFLNPLIYSLRNKDMKDALKRVLGLTVS
QN (SEQ ID NO: 323)

ATGTTCTTTATTATTCACTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCAGAA
CAGAACAAATGCATTTTGTGACTGAGTTTGTCTCCTCCTGGGTTTCCATGGTCAAAGGGAGATG
CAGAGCTGCTTCTTCTCATTCATCCTGGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC
TATTGTCTGTGCACTGAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTTCTGGGA
AACTTTGCCTTTCTAGAGATCTGGTACATTTCTCCACTGTCCCAAACATGCTAGTCAATAT
45 CCTCTCTGAGATTAAAACCATCTCCTTCTCTGGTTGCTTCTGCAATTCTATTCTTTTTTTC
ACTGGGTACAACAGAGTGTTTTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTTCCCT
TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCCATTTGTTGCACTGGC
50 CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC
TCTGGTGTGGTCAACTAAAGCTTTCTCCACATGTGGGTCCCACCTAATGGTGGTGTCTC
TATTCTATGGAACCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCTTATCTAT
55 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCTGGGGTTAACAGTTAGC
CAAACTGA (SEQ ID NO: 324)

AOLFR177 sequences:

- MSFFVLDLRPMNRSATHIVTEFILLGFPGCWKIQIFLSLFLVIYVLTLLGNGAITYAVRCNPLLH
 TPMYFLLGNFAFLEIWYVSSIPNMLVNLSKTKAISFSGCFQFYFFSLGTTTECLFLAVMAYD
 5 RYLAICHPLQYPAIMTVRFCGKLVSCFWLIGFLGYPIPIFYISQLPFCGPNIDHFLCDMDPLMAL
 SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLTAVFQVPSAAGRRAKAFSTCGSHLVVVSIFYG
 TVMVMYVSPTYGIPTLLQKILTLVYSVTTPLFNPLIYTLRNKDMKLALRNVLFGMRRQNS
 (SEQ ID NO: 325)
- 10 ATGTCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG
 AGTTTATTCTCCTGGGATTCCCTGGTTGCTGGAAGATTGAGATTTTCCTCTTCTCATTGTTT
 TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA
 ACCCACTACTACACACCCCATGTACTTTCTGCTGGGAAATTTGCCTTCTTGAGATCTGG
 TATGTGCTCCTCACTATTCCTAACATGCTAGTCAACATTCTCTCCAAGACCAAGGCCATCTC
 15 ATTTCTGGGTGCTTCTCCAGTTCTATTCTTCTTTTCACTGGGAACAACCTGAATGTCTCT
 TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCTGC
 CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCTTG
 GATACCCAATTCCCATTTTCTACATCTCCCAACTCCCTTCTGTGGTCTTAATATCATTGAT
 CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCAGCTCCCATAACTGAT
 20 AATGTATTTTCTATACTCAGAGCTCCCTTGCTCTTTTCACTAGTATGTACATTCTTCGA
 TCCTATATCCTGTTACTAACAGCTGTTTTTCAGGTCCTTCTGCAGCTGGTCGGAGAAAAG
 CCTTCTCTACCTGTGGTTCTCATTTGGTTGTGGTATCTCTTTTCTATGGGACAGTCATGGTA
 ATGTATGTAAGTCCTACATATGGGATCCCAACTTTATTGCAGAAGATCCTCACACTGGTAT
 ATTCAGTAACGACTCCTCTTTTAATCCTCTGATCTATACTCTTCGTAATAAGGACATGAAA
 25 CTCGCTCTGAGAAATGTCCTGTTTGAATGAGAATTCGTCAAAATTCGTGA (SEQ ID NO:
 326)

AOLFR178 sequences:

- MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNLILLTVTSDPHLHSPMYFLL
 30 ANLSFIDLGVSSVTSFKMIYDLFRKHEVISFGGCIQIFFIHVIGGVEMVLLIAMAFDRYVAICKP
 LQYLTIMSPRMCMFFLVAAWVTGLIHSVVQLVFVNLPFCGPNVSDSFYCDLPRFIKLACTDSY
 RLEFMVTANSGLISLGSFFILIISYVVILTVLKHSSAGLSKALSTLSAHVSVVVLFFGPLIFVYTW
 PSPSTHLDKFLAIFDAVLTPVLNPIYTFRN (SEQ ID NO: 327)
- 35 ATGGTTGGGGCAAATCACTCCGTGGTGTGAGAGTTTGTGTTCTGCGGACTCACCAATTCCT
 GGGAGATCCGACTTCTCCTCCTTGTTCTCCTCCATGTTTACATGGCCAGTATGATGGGA
 AACTCTCTCATTTTGCTCACTGTGACTTCTGACCCCTCACTTGCCTCCCATGATTTTCT
 GTTAGCCAACCTCTCCTTCATTGACCTGGGTGTTTCTCTGCTCACTTCTCCCAAAATGATTT
 ATGACCTGTTGAGAAAGCACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT
 40 CATCCACGTCATTGGCGGTGTGGAGATGGTGTCTCATAGCCATGGCCTTTGACAGATAT
 GTGGCCATATGTAAGCCCTCCAGTACCTGACCATTATGAGCCCAAGAATGTGCATGTTCT
 TCTTAGTGCTGCTGGGTGACCGGCCTTATCCACTCTGTAGTTCAATTGGTTTTTGTAGTA
 AACTTGCCCTTCTGTGGTCTAATGTATCGGACAGCTTTTACTGTGACCTTCTCGGTTTCAT
 CAAACTTGCCCTGCACAGACAGTACCGACTGGAGTTTCATGGTTACAGCCAACAGTGGATTCT
 45 ATCTCTCTGGGCTCCTTCTTCATACTGATCATTTCTATGTGGTTCATATCTCACTGTTCT
 GAAACACTCTTCAGCTGGTTTATCCAAGGCTCTGTCCACCCTTTCAGCTCAGTCAGTGTG
 GTAGTTTTGTTCTTTGGTCTTTGATTTTTGTCTATACGTGGCCATCTCCCTCCACACACCT
 GGATAAGTTTCTGGCCATCTTTGATGCAGTTCTCACTCCTGTTTTAAATCCTATCATCTACA
 CATTCAGGAATTGA (SEQ ID NO: 328)

50

AOLFR179 sequences:

- MNGMNHSVVSEFVFMGLTNSREIQLLLFVFSLLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL
 ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP
 LHYLTIMSPRMCLYFLATSSIIIGLIHSLVQLVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL
 55 EFMVTVNSGLISVGSFVLLVISYIFILFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW
 PSPTSHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVAMRRRLCSRLAHFTKIL (SEQ ID NO: 329)

ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTTCATGGGACTCACCAACTCAC
 GGGAGATTGAGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA
 AACCTTGTCAATTGTATTCATGTAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCTT
 5 CCTGGCTAACCTCTCAATCATTGATATGGCATTGCTCAATTACAGCCCCTAAGATGATTT
 GTGATATTTTCAAGAAGCACAAGGCCATCTCTTTTCGGGGATGTATTACTCAGATCTTCTT
 TAGCCATGCTCTTGGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAC
 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAAATGTGTCTATACT
 TTTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTGTGGTA
 10 GATTACCTTTTTGTGGTCCTAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT
 CAGACTTGCCTGTACCAACACCCAAGAACTGGAGTTTCATGGTCACTGTCAATAGTGGACTC
 ATTTCTGTGGGCTCCTTTGCTTGTGTAATTTCTACATCTTCATTCTGTTCACTGTTTG
 GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTCTACCCTGTCAGCTCATGTCACTGTG
 GTCATCTTGTCTTTGGGCCACTGATGTTTTCTACACATGGCCTTCTCCACATCACACCT
 15 GGATAAATATCTTGCTATTTTTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA
 CATTGAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGCTTGGCGCATT
 TTACAAAGATTTTGTA (SEQ ID NO: 330)

AOLFR180 sequences:

20 MTKMYAIYIKNLNYFSFLIVQCLQPTMAIFNNTTSSSNFLLTAFPGLECAHVWISIPVCCLYTI
 ALLGNSMIFLVIITKRRHLKPMYFLSMLAAVDLCLTITLPTVLGVLWFHAREISFKACFIQMF
 FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLPLLVAINTVSF
 HGGHLSHPFCYHPEVIKYTYSKPWISSFWGLFLQLYLNGLDVLFILFSYVLILRTVLGIVARKK
 QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLPPVLNPIIYSLKTKTIR
 25 QAMFQLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTTCTTTCCTCATAGT
 TCAGTGCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCTCAAACCTTCC
 TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
 30 CTCTACACCATTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTATCATTACTAAGCGGA
 GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
 ATTACGACCCCTCCCACTGTGCTTGGTGTCTCTGTTTCATGCCCCGGGAGATCAGCTTTAA
 AGCTTGCTTCATTCAAATGTTCTTTGTGCACTGCTTCTCCTTGCTGGAGTCCCTCGGTGCTGG
 TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCTC
 35 ACAGACAGGATGGTCCTGGTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTTCTTAC
 TTCCCTTCTTGTAGCCATAAACACTGTGTCTTTTCATGGGGGTCACGAGCTTTCCCATCCA
 TTTTGCTACCAACCCAGAAAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTT
 GGGGACTGTTTCTTCACTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTTCTCCTAT
 GTCCTGATCCTCCGTAAGTGTCTGGGCATTGTGGCCCGAAAGAAGCAACAAAAAGCTCTCA
 40 GCACTTGTGTCTGTACATCTGTGCAGTCACTATTTTCTATGTGCCACTGATCAGCCTCTCT
 TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGCTCTGTAGCACTTTGGCCAATATTTA
 TCTGCTCTTACCACCTGTGCTGAACCTTATCATTACAGCTTGAAGACCAAGACAATCCGC
 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTAAATGTGAGGGGTCTTA
 GGGGAAGATGGGATTGA (SEQ ID NO: 332)

45

AOLFR181 sequences:

MSVLNNSEVKLFLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMMYYFLAML
 AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLMSLDRFLAIHNPLR
 YSSILTSNRVAKMGLILAIRSILLVIPFPFTRLRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV
 50 IYGFIALCTMLDLALIVLSYVLILKTLISLASLAERLKALNTCVSHICAVLTFYVPIITLAAMHFF
 AKHKSPLVVILIADMFLVPLMNPVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTTCTGATTGGGATCCCAGGACTGG
 AACATGCCACATTTGGTTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGC
 55 AACTGCACCATTTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT
 CCTTGCCATGTTGGCTGTCTGACATGGGCCTGTCCCTCTCCTCCCTTCCATCATGTTGA

GGGTCTTCTTGTCAATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATTTCTC
 ATTCATGGATTCACTGTGCATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT
 TGCCATTACAAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAAATG
 GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTCACCTTAAGGAG
 5 ATTAATAATTGTCAAAGAATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA
 AGCTGGCCTGCTCTGACAACAAGACCAATGTCATCTATGGCTTCTTCATTGCTCTCTGTACT
 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT
 TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATAACCTGTGTCTCCACATCTGTGCTGTG
 CTCACCTTCTATGTGCCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCAGAAAA
 10 GCCCTCTGTGTGATCCCTTATTGCAGATATGTTCTTGTGGTGCCGCCCTTATGAACCC
 ATTGTGTAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
 GTATGTGGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

15 MTLGSLGNSSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYLFL
 SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSELESSVLLSMAFDRFVAICHP
 LHYVSILNTVIGRIGLVSLGRSVALIFPLPMLKRFPCGSPVLSHSYCLHQEVMKLACADMK
 ANSIYGMFVIVSTVIGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
 IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVYSVKTKQIRDRVTHAFY (SEQ ID NO: 335)

20 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCCTGCTGAGTG
 GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT
 GGTTTCCATCCCGGGCAACTGCACAATTCTTTTATCATTAAAAACAGAGCGCTCACTTCAT
 GAACCTATGTATCTCTTCTGTCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC
 25 TCTCCCTACAGTCCCTGGGCATCTTTTGGGTTGGAGCACGAGAAATTAGCCATGATGCCTGC
 TTTGCTCAGCTCTTTTCATTCACTGCTTCTCCTTCTCGAGTCTCTGTGCTACTGTCTATG
 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC
 AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTGCTAGTGTAGCACTCATTTTCCATTA
 CCTTTTATGCTCAAAAGATTCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT
 30 CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT
 GTTTGTCATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTCTTATGCTCTGA
 TCCTGCGCACCGTGTCTGTCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG
 TGTTTCCACATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCATCC
 ATCGCTTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTCATGGGTTTCATGTATCTTCT
 35 CTTTCTCCTGTGATGAATCCCATTTGTCTACAGTGTGAAGACCAAAACAGATCCGGGATCGA
 GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

AOLFR183 sequences:

40 MTNLNASQANHRNFILTGIPGTPDKNPWLAFPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYFYFL
 SILALTDVSLSMSTLPSMLSIFYWFNAPQIVFDACIMQMFFIHVFGIVESGVLVSMFDRFVAIRN
 PLHYVSILTHDVIRKGTISVLTRA VCVVFPVPFLIKCLPFCHSNVLSHSYCLHQNMRLACASTR
 INSLYGLIVIFTLGLDVLLTLLSYVLTLKTVLGIVSRGERLKTLSLCLSHMSTVLLFYVPMGA
 ASMIHRFWEHLSPVVHVMADIYLLLPVLNPVYSVKTKQI (SEQ ID NO: 337)

45 ATGACGAACTTGAATGCATCACAGGCCAACCCCGTAACCTTCTGACAGGTATCCCAG
 GAACGCCAGACAAGAACCCATGGTTGGCCTTTCCCTGGGATTTCTCTACACACTCACACT
 CCTGGGAAATGGTACCATCCTAGCTGTCACTCAAGGTGGAGCCAAGTCTCCATGAGCCACG
 TATTACTTCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC
 ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTTGATGCATGCATCATGCAGAT
 50 GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCTAGTGTCCATGGCCTTTGAC
 AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTGC
 AAAGACTGGAATATCTGTCTCACCCGGGCAGTCTGTGTGGTATTCCTGTGCCCTTCTCT
 ATAAAGTGCCCTACCCTTCTGCCATTCCAATGTCTTGTCTCATTCTACTGTCTTACCAAAA
 CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGTC
 55 ATCTTCACTGGGGCTCGATGTTCTCCTCACTCACTGTCTTATGTACTACCCTGAAGAC
 TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAAACCCCTCAGCACATGCCTCTCTCAC

ATGFTACCGTGCTCCTCTTCTATGTTCTTTTATGGGTGCTGCCTCCATGATCCACAGATT
TTGGGAGCATTTATCACCAGTAGTGACATGGTCATGGCTGATATATACCTACTGCTCCCG
CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

5 **AOLFR184 sequences:**

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTLPPLIAVYLLSALNGNTILWIALQPALHR
PMHFFLLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFIHVFSVMESSVLLAMSID
RALAICRPLHYPALLTNGVISKISLAISFRCLGLHLPFLLAYMPYCLPQVLTHSYCLHPDVARL
ACPEAWGAAYSLFVVL SAMGLDLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLSAVLLF
10 YIPMILLALINHP LIPITQHTHTLLSYVHFLPLINPILYSVKMKEIRKRLNRLQPRKVGGAGQ
(SEQ ID NO: 339)

ATGTCAACATTACCAACTCAGATAGCCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCCTCTGGTGGACATTGCCCTCATTGC
15 TGTCTACCTTCTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC
GCCCTGCACCGCCCAATGCACTTCTTCTCTTCTTCTGCTTAGTGTGTCTGATATTGGATTGGT
CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTTGTGGTGTCTCACACTGTCCCTGCC
TCAGCCTGCCCTTCTACAGATGGTTTTATCCATGTCTTTCTGTCTATGGAGTCTCTGTCTT
GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC
20 CTCACCAATGGTGTAAATTAGCAAAATCAGCCTGGCCATTTCTTTTCGATGCCTGGGTCTCC
ATCTGCCCCCTGCCATTCTGTGGCTACATGCCCTACTGCCTCCACAGGTCTTAACCCAT
TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCAGAAGCTTGGGGTGCAGCCT
ACAGCCTATTGTGGTTCTTTACGCCATGGGTTTGGACCCCTGCTTATTTCTTCTCCTAT
GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT
25 CAAACCTGTGCTGCCACCTCTCTGCAGTGCTCCTCTTCTATATCCCTATGATCCTCCTGGC
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCCTATGTCC
ATTTCTTCTTCTCCTCCATTGATAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA
AAGAGAATACTCAACAGGTTGCAGCCCAGGAAGGTGGGTGGTGTCTCAGTGA (SEQ ID NO:
340)

30

AOLFR185 sequences:

MFYPILNDISTKNNSNIMSCCNILFIKTVEIILVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR
VDCVPSRDHINQSMVLASGNSSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR
IDHTLHEPMYLF LAMLAITDLVLSSTQPKMLAIFWFAHEIQYHACLIQVFFIHAFSSVESGVL
35 MAMALDCYVATCFPLRHSSILTPSVVIKLGITVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC
EHMAVLKLVCA DTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
SHICVILALYPALFSFLT YRFGHDVPRVVHILFANLYLLIPMLNPIIYGVRTKQIGDRVIQGCCG
NIP (SEQ ID NO: 341)

40 ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCTGTT
GTAACATATTATTTATTAACAGTTGAAATTATTCTAGTTTATAATCAAACCCAATCACC
CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAATAACACTTGTTTGGATTGTT
ATCATCTGCAGAGAGTAGATTGCGTTCCCAGCAGAGACCATATTAACAGTCCATGGTGCT
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCTTCTCATCTGCTTGGAAATCCAGGCCTG
45 GAGAGTTTCCAGTTGTGGATTGCCTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTTGG
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC
TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCTCTCCTCACTCAACCTAAGATGTT
GGCCATATTCTGGTTTCTATGCTCATGAGATTAGTACCATGCCTGCCTCATCCAGGTGTTCT
TCATCCATGCCCTTTCTTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACTGCTAC
50 GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTGCTGATCAAAC
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCTTCTGCTTCATGGTGTG
TAGGATGCCCTTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG
CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTGTGGCCTTCT
CTGTGGCTGGCTTTGATATGATTGTCATTGGTATGTCATACGTGATGATTTTGAGAGCTGT
55 GCTTCAGTTGCCCTCAGGTGAAGCCCGCCTCAAAGCTTTTAGCACACGTGCCTCCCATATC
TGTGTCATCTTGGCTCTTATATCCCAGCCCTTTTCTTCTCCTCACCTACCGCTTTGGCCAT

GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT
CAACCCCATCATTTATGGAGTTAGAACCAACAGATCGGGGACAGGGTTATCCAAGGATG
TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)

5 **AOLFR186 sequences:**

MSNASLVTAFLTGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAIISYPL
RYTSMMSGSRCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTSA
NVMVIFVDIGIVASGCFVLIVLSYVSVCSILRRTSDGRRRAFQTCASHCIVVLCFVPCVVYLR
10 PGMDAMDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKLRDKVAHPQRK (SEQ ID NO:
343)

ATGTCCAACGCCAGCCTCGTGACAGCATTCATCCTCACAGGCCCTTCCCCATGCCCCAGGGC
TGGACGCCCTCCTCTTTGGAATCTTCTCGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
15 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCTGCGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG
20 CCACCGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
AAGTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT
GGCCTCAGGCTGCTTTGTCCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCTGC
GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT
25 GGTCTTTGCTTCTTTGTTCCCTGTGTTGTCATTTATCTGAGGCCAGGCTCCATGGATGCCA
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTTAGAGACAAAGTAGCACAT
CCTCAGAGGAAATAA (SEQ ID NO: 344)

30 **AOLFR187 sequences:**

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGIPGLEQLHIWLSIPFCIMYIAALEGNLILI
CVILSQAILHEPMYIFLSMLASADVLLSTTTMPKALANLWLGYSHISFDGCLTQKFFHFLFIHSA
VLLAMAFDRYVAICSPLRVYVITLSKVIGKIVTATLSRSFIIMFPSIFLLEHLHYCQINIAHTFCEH
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV
35 ILLFYVPALFSVFAYRFGGRSIPCYVHILLASLYVVPMLNPVIYGVRTKPILEGAKQMFSNLAK
GSK (SEQ ID NO: 345)

ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG
CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCTCACTGGCATCCCTGGGCTGGA
40 GCAACTACATATCTGGCTGTCCATCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC
AATGGCATCCTAATTTGTGTATCCTCTCCCAGGCAATCCTGCATGAGCCCATGTACATAT
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG
GCCAATTTGTGGCTAGGTTATAGCCACATTTCTTTGATGGCTGCCTCACTCAAAAGTTCTT
CATCACTTCTCTTCACTTCACTCTGCTGTCTGCTGGCCATGGCCTTGACCGCTATGTGG
45 CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCATTGGGAAGATCGT
CACTGCCACCCTGAGCCGCAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC
TGCATATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA
TCTGTCTGTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTTCTCTCCA
CAGGCCTGGACATCATGCTTATTACTGTTTCTACATCCACATCCTCCAAGCAGTCTTCCGC
50 CTCCTTTCTCAAGATGCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCAT
CCTACTCTTCTATGTCCCTGCCCTTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA
TCCCATGCTATGTCCATATTCTCTGGCCAGCCTCTACGTTGTCTTCTCCTATGCTCAAT
CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTCA
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

55

AOLFR188 sequences:

MFPSLCPCVLLVQLPLMNENMQCFVFCSDSLLRMMVSRFIHVFPVKMKRIIVGGYSKHFFSN
 ELLCVRPWSGKTWSIRHHIFDMELLTNNLKFITDPFVCRLRHLSPSEEHMKNNVTEFILL
 GLTQNPGEQKVLFVTFLLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLFSIDTVYSTAFAPK
 5 MIVDLLSEKKTISFQGCMAQLFMDHLFAGAEVILLVVMAYDRYMAICKPLHELITMNRRCVIL
 MLLAAWIGGFLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC
 AVTFFTILLSYGVILHSLKTSLEGKRKAFTYCASHVTVVILFFVPCIFLYARPNSTFPIDKSMTV
 VLTFTITPLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

10 ATGTTCCCTCCCTGTGTCCATGTGTTCTCCTGTTCACCTCCCACTTATGAATGAGAACAT
 GCAGTGTTTTGTCTTCTGTGATAGTTGCTGAGAATGATGGTTTCCCGCTTCATCC
 ATGTCCCATTTGTAATAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC
 TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT
 TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCCTTTTGTGTAGGC
 15 TCCGACACCTGAGTCCAACACCTTCAGAAAGACACATGAAAAATAAGAACAAATGTGACTG
 AATTTATCCTCTTAGGGCTCACACAGAACCTGAGGGGCAAAAGGTTTTATTTGTCACATT
 CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC
 AGCCAGTCCCTGGGTTCCCATGTACTTTTTCTGGCTTCTTTATCATTATAGATACCGT
 CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATTT
 20 CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTATTTGCTGGTGCTGAAGTCATT
 CTTCTGGTGGAATGGCCTATGATCGATACATGGCCATCTGTAAGCCTCTTCATGAATTGA
 TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTTCT
 TCACTCATTTGGTCAATTTCTCTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG
 ACAACTTCCTGTGTGATTTGTATCCCTTATTGAAACTTGCTTGACCAATACCTATGTCACT
 25 GGGCTTTCTATGATAGCTAATGGAGGAGCGATTTGTGCTGTACCTTCTTCACTATCCTGC
 TTTCTATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGGAAGGGAAACGAAAAGC
 TTTCTACACCTGTGCATCCACGTCACCTGTGGTCATTTTATTCTTTGCTCCCTGTATCTTCT
 GTATGCAAGGCCCAATTCTACTTTTCCCATGATAAATCCATGACTGTAGTCTAACTTTTA
 TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT
 30 GAGGAAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA
 (SEQ ID NO: 348)

AOLFR189 sequences:

MQQNNVPEFILLGLTQDPLRQKIVFVIFLYMGTVVGNMLIIVTIKSSRTLGSMPYFFLYLSF
 35 ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDRYVAICKPLRYP
 TIMSQQVCHILIVLAWIGSLIHSTAQIILALRLPFCGPYLDHYCCDLQPLLKLACMDTYMINLLL
 VNSGAICSSSFMLIISYIVILHSLRNHSAKGGKALSACTSHIIVILFFGPCIFIYTRPPTTFPMD
 KMAVAFYITIGTPFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

40 ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA
 GGCAGAAAATAGTGTGTGTAATCTTCTTAATTTTCTATATGGGAACTGTGGTGGGGAATAT
 GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGTACTTCTTTCTA
 TTTTATTTGTCTTTGCAGATTCTTGCTTTTCAACTTCCACAGCCCCTAGATTAATTGTGGA
 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTGCACTA
 45 CATTATTTGGCTGCATGGAGATCTTTGTCTCATTCTCATGGCTGTTGATCGCTATGTGGC
 CATCTGTAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT
 GTTCTTGCTGGATAGGGTCTTTAATACACTCTACAGCTCAGATTATCCTGGCCTTAAGATT
 GCCTTTCTGTGGACCCTATTTGATTGATCATTATTGCTGTGATTGTCAGCCCTTGTGAAAC
 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG
 50 CTCAAGTAGTTTCATGATTTTGATAATTTTCATATATTGTCATCTTGCAATCACTGAGAAACC
 ACAGTGCCAAAGGGAAGAAAAAGGCTCTCTCCGCTTGACAGTCTCACATAATTGTAGTCAT
 CTTATTCTTTGGCCCATGTATATTCATATATACACGCCCCCGACCACTTTCCCCATGGACA
 AGATGGTGGCAGTATTTTATACTATTGGAACACCCTTTCTCAATCCACTCATCTACACATCT
 GAGGAATGCAGAAGTGAAAAATGCCATGAGAAAG (SEQ ID NO: 350)

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AOLFR190 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
YAQTMPRRLCICLVLYSYTGGFVNAHLTSNTFTLDFCGDNVIDDFCDVPPLVKLACSVRESYQ
5 AVLHFLLASNVISPTVLILASYLSIITLIRIHSTQGRIKVFSTCSSHLISVTLYYGSILYNYSRPSSS
YSLKRDKMVSTFYTMLFPMLNPMIYSLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGACTGAGTTCATCCTGCTGGGCTTCACCACAGATCCAG
GGATGCAACTGGGCCTCTTTGTGGTGTTCTGGGTGTGTACTGTCTGACTGTGGTAGGAAG
10 TAGCACCCCTCATCGTGTGATCTGTAATGACTCCCGCCTACACACACCCATGTATTTGTCA
TTGGAAATCTGTCATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG
ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCAAGTTCTTCTCTGC
CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC
ATCTCCAAGCCCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT
15 ATATTCCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTACATTG
GATTTTTGTGGTGACAATGTCATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT
GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC
ATCTCCCCCTACTGTGCTCATCCTTGCCTCTTACCTCTCCATCATCAACCACCATCCTGAGGAT
CCACTCTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCACCTGATCTCCGTTA
20 CCTTATACTATGGCTCCATTCTCTACAATACTCCCGGCCAAGTTCCAGCTACTCCCTCAAG
AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCATGTTGAATCCCATGATCTA
CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA
(SEQ ID NO: 352)

AOLFR191 sequences:

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVTYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
 FIDVCYISSVTPKMLSNLLQEQQTITFVGCIQYFIFSTMGLSESLMTAMAYDRYAAICNPLLYS
 SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDTFFVQV
 5 MTAILTMFFGLASALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSGIFVYLRSSS
 GGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT
 TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC
 10 TGGAACTCTCCCTCATTGTTTAAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT
 CTTCCTCAGTAACCTGTCCTTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC
 TCTCCAACCTCTTACAGGAACAGCAAATATCACITTTGTTGGTTGTATTATTCAGTACTTT
 ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
 ATGCTGCCATTTGTAACCCCTGCTCTATTTCATCCATCATGTCACCCACCCTCTGTGTTTGG
 15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTGCT
 TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCCAACTGT
 TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTT
 TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
 TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC
 20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT
 CTTCAAGCTTTGACAGATTTGCATCTGTTTCTACACTGTGGTCATTCCCATGTTAAATCCC
 TTGATTTACAGTTTGAGGAACAAAGAAATTAAAGATGCCTTAAAGAGGTTGCAAAAGAGA
 AAGTGCTGCTGA (SEQ ID NO: 354)

AOLFR192 sequences:

MENNTEVTEFILVGLTDDPELQIPLFIVFLFIYLITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
 DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMA YDRYAALCKPLHY
 TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPPLLTLSCDNYISEM
 VIFFVVGFNDFSLVILISYLFIFITIMKMRSPGQRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS
 30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA
 CTGCAGATCCCCTCTTCATAGTCTTCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT
 GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCTCA
 35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG
 GTTCTCAGAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATCTTCTTCTTTG
 TAGCCTTTATCACTGCAGAAAGTTTCTCCTGGCATCAATGGCCTATGACCGCTATGCAGC
 ATTGTGTAAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC
 ATAGGCTCCTACATCTGTGGTTTCTGAATGCATCCATTCTACTGGGAACACTTTCAGGC
 40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTTCTGTGATGCTCCTCTCTTGA
 CTCTCATGTTTCAGACAACTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG
 ACCCTTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTTATCACCATCATGAAG
 ATGCGCTCACCTGAAGGACGCCAGAAGGCCTTTTCTACTTGTGCTTCCCACCTTACTGCAG
 TTTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTTCATG
 45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
 TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAAGACTGTAGGGAAGGCAA
 AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

MENKTEVTQFILLGLTNDSELQVPLFITFPFIYIITLVGNLGIIVLIFWDSCLHNPMYFFLSNLSLV
 DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMA YDRYA AAVCKPLHY
 TTTMTTIVCARLAIGSYLCGFLNASIHTGDTFSLSFCKSNEVHHFFCDIPAVMVLSCSDRHISEL
 VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFIAVGIFYGTIIFMYLQPSSSH
 SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSAFKKVVEKAKLSVGWSV (SEQ ID NO:
 55 357)

ATGGAAAATAAGACAGAAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA
 CTGCAGGTTCCCTCTTTATAACGTTCCCTTCATCTATATTATCACTCTGGTTGGAAACCT
 GGGAATTATTGTATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTTTCTCA
 GTAACCTGTCTCTAGTGGACTTTTGTCTACTTTCAGCTGTCACTCCCATCGTCATGGCTGGA
 5 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT
 AGCTTTTGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA
 TAGGCTCCTACCTCTGTGGTTTCCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC
 TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTCTGTGATATTCAGCAGTCATGGTTCT
 10 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTTCTTATTTATGTTGTGAGCTTCAATATCT
 TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTATCACCATCCTAAAGATG
 CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATTGCAGTCGG
 CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
 CAGACAAAATGGCACCTGTGTTCTATAACAATGGTCATCCCCATGCTGAACCCCTCTGGTCTA
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

MERQNSQCVVEFILLGFSNYPELQGQLFVAFVLVIYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL
 20 SVVDLSFSAVIMPEMLVVLSTEKTTISFGGCF AQMYFILLFGGAECFLLGAMAYDRFAAICHPL
 NYQMIMNKGVMKLIIFSWALGFMLGTVQTSWVSSPFCGLNEINHISCETPAVLELACADTF
 FEIYFTGTFLILVPFLLILLSYIRVLFALIKMPSTTGRQKAFSTCAHLTSVTLFYGTASMTYLG
 PKSGYSPETKKVMSLSYSLLTPLLNLIIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:
 359)

25 ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
 CTGAGCTCCAGGGGAGCTCTTTGTGGCTTTCTGGTTATTTATCTGGTGACCCTGATAGG
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT
 TTCTCCTGAACCTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT
 30 GGTGGTCTCTCTACTGAAAAAATAACAATTTCTTTTGGGGGCTGTTTGCACAGATGTAT
 TTCATCCTTCTTTTGGTGGGGCTGAATGTTTCTTCTGGGAGCAATGGCTTATGACCGATT
 TGCTGCAATTTGCCATCCTCTCAACTACCAAATGATTATGAATAAAGGAGTTTATGAAA
 TTAATTATATTTTCATGGGCCTTAGGTTTATGTTAGGTACTGTTCAAACATCATGGGTATC
 TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT
 35 TAGAAGTGCATGTGCAGACACGTTTTTGTGAAATCTATGCATTACAGGCACCTTTTTG
 ATTATTTTGGTTCTTTCTTGTGATACTCTTGTCTTACATTGAGTTCTGTTTGCCATCCTG
 AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCGCTCACCTCACAT
 CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC
 ACCGGAACCAAGAAAGTGATGTCTTGTCTTACTCACTCTGACACCACTGCTGAATCTG
 40 CTTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGCTTTGATGAAATTATGGCGAAGG
 CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

MIVQLICTVCFNAVNTFHVRSFDFLKADDMGEINQTLVSEFLLGLSGYPKIEIVYFALILVMY
 45 LVILIGNGVLIASIFDSHFHTPMYFFLGNLSFLDICYTSSSVPTLVSLISKRNISFSGCAVQMFF
 GFAMGSTECILLGMMAFDYVAICNPLRYPIILSKVAYVLMASVSWLSGGINSVQTLAMRL
 PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVPLMVIFFSYMFILYTLQMNSATG
 RRKAFSTCSAHLTVVIIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSLR
 NKDVKAADVLYLLNKKPIH (SEQ ID NO: 361)

50 ATGATTGTTTCAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTTCATGTTAGATC
 TTCTTTTGATTTCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTGTGTGAGAA
 TTTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT
 AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT
 55 CTCATTTTCACACACCAATGTACTTCTTCTGGGCAACCTCTCTTCTGGATATCTGCTAT
 ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCT

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAATGTCTGCT
 TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
 ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGAATAA
 ATTCAGCTGTGCAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA
 5 TCATTTTCGCATGTGAAATATTAGCTGTCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA
 TTATCACCATGGTGATATCAAATATGGCCTTCTGGTTCTTCCACTGATGGTCATTTTTTTC
 TCCTATATGTTTCATCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG
 CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT
 ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC
 10 AAGCTCATTTCTCTGTTTATGGGGTAGTGACACCCATGCTGAATCCTATACTCTATAGCTT
 GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTTGCTGAACAAAAAACCAATCACTA
 A (SEQ ID NO: 362)

AOLFR196 sequences:

15 MLESNYTMPTEFLVFGFTDYLPLRVTLFLVFLVYTLTMVGNILLIILVNINSSLPIMYYFLSNL
 SFLDISCSTAITPKMLANFLASRKSSPYGCALQMFFFAFADAECILILAAAMAYDRYAAJCNPLL
 YTTLMSSRRVCVCFVLAIFYSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPPLLALSCDTQINQL
 LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
 20 YSLDTDKVVAVFYTVVPMFNPFIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
 ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC
 TACCTCTCAGAGTCACACTGTTCTTGGTATTCCTTCTGGTATATACATTAACATATGGTCGGA
 AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTTCAAATCCCAGTATTATTT
 25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAAATGCTGG
 CAAACTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT
 CTTGCTTCTTTTGTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG
 CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT
 CATGTGTGTGGCATATTTCAAGTGAAGTACAACATCACTGGTCCATGTGTGCCCTCACATTC
 30 AGGCTGTCATTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCCACCTCTTCT
 GGCTTTATCATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGCTTCA
 TCCAGACGCACTTTTGTGGTAATATTTTCTTACTTCTGCATCCTCATCACTGTGTTG
 AGCACTCAAGTCTCAGGTGGCAGAAAGCAAAACATTCTCCACTTGTGCTTCCACCTCATAG
 CAGTCACTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCCACCACTAGCTATTCC
 35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAA
 TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
 TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAAGAATAGTCAATATCTAA (SEQ ID NO:
 364)

AOLFR197 sequences:

40 MCYLSQLCLSLGEHTLHMGMRHTNESNLAGFILLGFSQDYPQLQKVLVFLILILYLLTILGNTTI
 ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS
 TECVLLALMSCDRYVAVCRPLHYTVLMHHLCLMALASMAWLSGIATTLVQSTLTLQLPFCGH
 RQVDHFICEVPVLIKACVGTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSATRRQKAF
 45 GTCFSLTLVVTIFYGTIIFMYLQPAKSRSDQGKFSVLFYTVVTRMLNPLIYTLRIKEVKGALKK
 VLAKALGVNLI (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
 TGAGACATACCAATGAGAGCAACCTAGCAGTTTCATCCTTTTAGGGTTTTCTGATTATCC
 50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTTGGGGA
 ATACCACCATCATCTGGTTTCTCGTCTGGAACCCAAGCTTCATATGCCGATGTATTTCTTC
 CTTTCTCATCTCTCCTTCTGTACCGCTGCTTACCAGCAGTGTTATTTCCCACTCTCTGGT
 AAACCTGTGGGAACCCATGAAAACTATCGCCTATGGTGGCTGTTTGGTTACCTTTACAAC
 TCCCATGCCCTGGGATCCACTGAGTGCCTCTTGGCTCTGATGTCTGTGACCGCTATGT
 55 GGCTGTCTGCCGCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG
 CATCTATGGCATGGCTCAGTGAATAGCCACCACCCTGGTACAGTCCACCCTCACCTGCA

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC
AAGCTGGCTTGTGTGGGCACACGTTTAAACGAGGCTGAGCTTTTGTGGCTAGTATCCTTT
TCCTTATAGTGCCTGTCTCATTTCATCCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTG
AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTGCGGACCTGCTTCTCCACCTGACA
5 GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT
CCAGGGACCAGGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA
GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMAYDRYAAVCKP
LHYTTMTASVGACLALGSYVCGFLN~~AS~~HFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH
TSEVILVMSSFNIFVLLVIFISYLFIFITILKMHSAGHQAALSTCASHFTAVSVFYGTVIFITYLQ
15 PSSSHSMDTDKMASVFYAMIIPMLNPVVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC
TACAGATCCCCCTCTTATCTTGTTCACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
GGGATGATGTTGCTGATCCTGATGGACTCTTGTCTCCACACCCCCATGTACTTTTTCTCAG
20 TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG
TTCCTTAGAGGAGACAAGGTCACTCTCCTACAATGCATGTGCTGTTCAGATGTTCTTTGT
AGCCTTGCCACGGTGGAAAATTACTTGTGGCCTCAATGGCCTATGACCGCTATGCAGCA
GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC
TAGGCTCATATGTCTGTGGCTTCCTAAATGCCTCATTCCACATTGGGGGCATATTCACTCTC
25 TCTTTCTGTAAATCCAATCTGGTACATCATTCTTTCTGTGATGTTCCAGCAGTCATGGCTCT
GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTATGTCAAGCTTTAATATCT
TTTTTGTCTCTTAGTTATCTTTATCTCCTACTTGTTCATATTATCACCATCTTGAAGATGC
ATTCACTAAGGGACACAAAAAGCATTTGCCACCTGTGCCCTCACTTCACTGCAGTCTC
CGTCTTCTATGGGACAGTAATCTTCATCTACTTGCAGCCAGCTCCAGCCACTCCATGGAC
30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCTGTGGTCT
ACAGCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTGAGAAGGCAAAAAT
TTCTATAA (SEQ ID NO: 368)

AOLFR199 sequences:

35 MDTGNKTLPODFLLGFPGSQTQLQLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
NLSFLEIWTYTTAAVPKALAILLGRSQTISFTSCLLQMYFVFLGCTEYFLLAAMAYDRCLAICYP
LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFFCDIAPWIALACTNTQA
VELVAFVIAVVVILSSCLITFVSYYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
TSIKDALDLIKAVHVLNTVVTPLNPFITYTLRNKEVRETLLKKWKGK (SEQ ID NO: 369)

40 ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCCTGGTTCTC
AAACTCTTCAGCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT
AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCCATGTACTTCTT
TCTGAGCAACCTCTCCTTCTGAGATTTGGTATACCACAGCAGCAGTGCCCAAAGCACTG
45 GCCATCCTACTGGGGAGAAGTCAGACCATATCATTTACAAGCTGTCTTTGCAGATGTACT
TTGTTTTCTCATTAGGCTGCACAGAGTACTTCCTCCTGGCAGCCATGGCTTATGACCGCTGT
CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
TGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAGTGCCACAGCCCTCATCAG
TGGCCTGTCCCTCTGTGGCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCCTGGA
50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT
GGTTATCCTGAGTTCATGCCTCATCACCTTTGTCTCCTATGTGTACATCATCAGCACCATCC
TCAGGATCCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC
CGTGGTGCTCATTGGTATGGGTCCACAGTTTTCTTCACGTCCGCACCTCTATCAAAGAT
GCCTTGGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTTAAACC
55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

MTRKNYTSLTEFVLLGLADTLELQIILFFLVITYTLTVLGNLGMILLIRIDSQ LHTPMYFFLANL
 SFVDVCNSTTTITPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL
 5 YSLIMSRTVYLKMAAGFAAAGLLNFMVNTSHVSSLSFCDSNVIIHFFCDSPPLFKLSCSDTILKE
 SSSILAGVNIVGTLLVILSSYSYVLFISFMSHSGEGRHRAFSTCASHLTAILFYATCIYTYLRPSS
 SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

 ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC
 10 TGGAGCTACAGATTATCCTCTTTTGTCTTTTCTTGTGATTTATACACTTACAGTACTGGGA
 AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTACACACCCCATGTATTTCTT
 CCTGGCTAACCTGTCCTTTGTGGACGTTTGTAACTCAACTACCATCACCCCAAAGATGCTG
 GCAGATTTATTATCAGAGAAGAAAAACCATCTCTTTGCTGGCTGCTTCTACAGATGTACT
 TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTTAATGGCCTATGACAGGTA
 15 TCGCGCCATATGTCGCCCCGCTGCTTACTCCTTGATCATGTCCAGGACCGTCTAGCTAAAA
 ATGGCAGCCGGGGCTTTTGTGTCAGGGTTGCTGAACCTTCATGGTCAACACAAGCCATGTCA
 GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCCACTT
 TTCAAGCTCTCTGTTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG
 TGAATATTGTGGGGACTCTGCTTGTCATCCTCTCCTCCTACTCCTACGTTCTCTTCTCCATT
 20 TTTTCTATGCATTGGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCACCTGA
 CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCCAGCTAC
 TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC
 CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAAGGCTTTAGCGAATGTAATTAGCA
 GGAAAAGGACCTCTTCTTTCTGTGA (SEQ ID NO: 372)

25

AOLFR201 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
 SFLDICYTTTSIPSTLVSFSLSERKTISLSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
 YPIIMSKDAYVPMAGSWIIGAVNSAVQSVFVQLPFCRNNIINHFTCEILAVMKLACADISDN
 30 EFIMLVATTILFILTPLLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIFYGTILFMYMKPKS
 KETLNSDDLDATDKIISMFGVMTMNMPLIYSLRNKDVKEAVKHLNRRFFSK (SEQ ID NO:
 373)

ATGGAATGGGAAAACCAACCATTTCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC
 35 CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
 AATGGTACTCTCATTTAATCAGCATCTTGGACCCTCACCTTACACCCCTATGTACTTCTT
 TCTGGGGAAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
 TGAGCTTCCTTTTCAAGAAAGAACCATTTCCCTTTCTGGCTGTGAGTGCAGATGTTTCT
 CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
 40 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
 TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTTTGTGGT
 ACAATTGCCCTTTCTGCAGGAATAACATCATCAATCATTTTACCTGTGAAATTCTGGCTGTC
 ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
 TGTTTATATTGACACCTTTGTTATTAATCATTTGTCTCTTACACGTTAATCATTTGTGAGCATC
 45 TTCAAAATTAGCTCTCCGAGGGGAGAAGCAAGCTTCTCTACCTGTTCAGCCCATCTGA
 CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA
 GACACTTAATTTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG
 ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA
 GTAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

50

AOLFR202 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
 SFLDICYTTTSIPSTLVSFSLSERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR
 YPIIMSKDAYVPMAGSWIIGAVNSAVQTVFVQLPFCRNNIINHFTCEILAVMKLACADISGN
 55 EFILLVTTTLFLLTPLLLIIVSYTLIILSIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

ETLNSDDLDATDKLIFIFRYVMTTPMMNPLIYSLRNKDVKEAVKHLLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACACACCATTCTGGTGGAATTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCTT
10 CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT
GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTAGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT
TGTTCTATTGACACCTTTGTTATTAATTAATGTCTCTTACACGTTAATCATTTTGAGCATC
15 TTCAAATTAGCTCTTCGGAGGGGAGAAGCAAACCTTCCTCTACCTGCTCAGCTCGTCTGA
CTGTGGTGATAACATTCTGTGGGACCATCTTCTCATGTACATGAAGCCCAAGTCTCAAGA
GACACTTAATTCAGATGACTTGGATGCCACTGACAAACTTATATTCATATTCTACAGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA
GTAAACACCTACTGAGAAGAAAAAATTTTAACAAGTAA (SEQ ID NO: 376)

20

AOLFR203 sequences:

25 MKRQNSQCVVEFILLGFSNPELQVQLFGVFLVIYVVTLMGNAITVIISLNQSLHVPMYLFLN
LSVVEVSFSAVITPEMLVVLSTKTMISFVGCFAQMYFILLFGGTECFLLGAMAYDRFAAICHPL
NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLCETPPVLELVCADTFLF
EIYAFTGTLIVMVPFLLILLSYIRVLFALKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLQ
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKRTLKLRWKVILHTF (SEQ ID NO: 377)

30 ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTCTAGTTATTTATGTGGTGACCCTGATGGG
AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT
TCTCCTGAACCTATCTGTGGTGGAGGTGAGTTTCAGTGCAGTCATTACGCCTGAAATGCT
GGTGGTGCTCTCTACTGAGAAAATATGATTTCTTTTGTGGGCTGTTTTGCACAGATGTAT
TTCATCCTTCTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTATGAAA
35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCGGTA
CTAGAGCTTGTGTGTGCAGACACCTTCTTATTTGAAATCTATGCCTTCACAGGCACCATTTT
GATTGTTATGGTTCCTTTCTTGTGATCCTCTTGTCTTACATTGAGTTCTGTTTGCCATCCT
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCTCTCACCTCACA
40 TCTGTGACCCCTGTTCTATGGCACAGCCAATATGACTTATTTACAACCCAAATCTGGCTACTC
ACCCGAAACCAAGAAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAAACTATGGCGAAGA
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

45 **AOLFR204 sequences:**

MEKKKNVTEFILIGLTQNPIMEKVTFVFLVLYMITLSGNLLIVVTTTTSQALSSPMYFFLTHLSL
IDTVYSSSSAPKLIVDSFQEKIISFNGCMAQYAEHIFGATEIILLTVMACDCYVAICKPLNYTT
IMSHSLCILLVAVAVWGGFLHATIQLFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDHTLGLFV
AVNSGFICLLNFLLVVSYVILRLSKNNSLEGRCKALSTCISHIIVVVLFFVPCIFVYLRSVTTLPI
50 DKAVAVFYTMVVPMLNPVVYTLRNAEVKSARKLWRKKVTSND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCAT
ATGGAGAAAGTCACGTTTGTAGTATTTTGGTTCTTTACATGATAACACTTTCAGGCAACC
TGCTCATTGTGGTTACCATTAACACAGGCTCTGAGCTCCCCCATGTACTTCTTCTG
55 ACCCACCTTTCTTTGATAGACACAGTTTATCTTCTTCTTACGCTCCTAAGTTGATTGTGGA
TTCTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

CACATTTTGGTGCTACTGAGATCATCCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG
 CCATCTGCAAACCTCTGAACTACACAACCATTATGAGCCACAGCCTGTGCATTCTCCTGGT
 GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTCAGATTCTCTTTACAGTATGG
 CTGCCCTTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGTGACTTGTACCCATTGTTAAA
 5 ACTTGTTTGCATAGACACTCATACCCTTGGTCTCTTTGTTGCTGTGAACAGTGGGTTTATCT
 GCTTATTAAACTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC
 AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTCACATCATAGTAGTTG
 TCTTATTCTTTGTGCCCTGTATATTTGTGTATCTGCGCTCAGTGACCACTCTGCCATTGAT
 AAAGCTGTTGCTGTATTTTATACTATGGTGGTCCCAATGTTAAATCCCGTGGTCTACACAC
 10 TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAAGTGACTTCAG
 ATAATGATTAA (SEQ ID NO: 380)

AOLFR205 sequences:

MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFILPGNFLIIFTIKSDPGLTAPLYFFLGNLAFL
 15 DASYSFTVAPRMLVDFLSAKKIISYRCITQLFHLHFLGGEGLLLVMAFDRIAICRPLHYPT
 VMNPRTCYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVPQVIKLACTDTFVVEL
 LMVFNGLMTLLCFLGLLASYAVILCRIRGSSSEAKNKAMSTCIITHIIVIFMFGPIFYTRFPRA
 FPAKDVVSLFHTVIFPLNPVIYTLRNQEVKASMKKVFKNHIA (SEQ ID NO: 381)

20 ATGGAAGCGAGAACAGAACAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT
 CAAGATATTCAGCTCCTGGTCTTTGTGCTAGTTTAAATATTCTACTTCATCATCCTCCCTGG
 AAATTTTCTCATTATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCT
 TTCTGGGCAACTTGGCCTTCCTGGATGCATCCTACTCCTTCACTGTGGCTCCCCGGATGTTG
 GTGGACTTCCTCTCTGCGAAGAAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT
 25 TCTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTGACCGCTA
 CATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTGATGAACCCTAGAACCTGCTATGCA
 ATGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCCT
 CCGCTTGCCTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCACAGGTC
 ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCC
 30 TGATGACACTCCTGTGCTTTCTGGGGCTTCTGGCCTCCTATGCAGTCATTCTTTGTGCATA
 CGAGGGTCTTCTTCTGAGGCAAAAAACAAGGCCATGTCCACGTGCATACCCATATCATTG
 TTATATTCTTCATGTTTGGACCTGGCATCTTCATCTACACGCGCCCCCTCAGGGCTTTCCCA
 GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTTCCTTTGTTGAATCCTGTCAATTA
 TACCCTTCGCAACCAGGAAGTGAAAGCTTCCATGAAAAAGGTGTTTAATAAGCACATAGC
 35 CTGA (SEQ ID NO: 382)

AOLFR206 sequences:

MANRNNVTEFILLGLTENPKMQKIIFVVSFVIYNAMIGNVLIVVTITASPSLRSPMYFFLAYLSFI
 DACYSSVNTPKLITDSLYENKTILFNGCMTQVFGHEHFRGVEVILLTVMAYDHYVAICKPLHYT
 40 TIMKQHVCSLLVGVSWVGGFLHATIQILFICQLPFCGPNVIDHFMCDLYTLINLACTNTHTLGLF
 IAANSFGICLLNCLLLLVS CVVILYSLKTHSLEARHEALSTCVSHITVVILSFIPCFVYMRPPATL
 PIDKAVAVFYTMITSMLNPLIYTLRNAQMKNAIRKLCRKAISSVK (SEQ ID NO: 383)

45 ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA
 ATGCAGAAAATCATATTTGTTGTGTTTTCTGTCTATCTACATCAACGCCATGATAGGAAATG
 TGCTCATTGTGGTCACCATCACTGCCAGCCCATCACTGAGATCCCCCATGTACTTTTTCTCTG
 GCCTATCTCTCCTTTATTGATGCCTGCTATTCTCTGTCAATACCCCTAAGCTGATCACAGA
 TTCACTCTATGAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA
 CATTTTTTCAGAGGTGTTGAGGTCACTCCTACTTACTGTAATGGCCTATGACCACTATGTGG
 50 CCATCTGCAAGCCCTTGCACTATACCACCATCATGAAGCAGCATGTTGTAGCCTGCTAGT
 GGGAGTGTGATGGGTAGGAGGCTTCTTCATGCAACCATACAGATCCTCTCATCTGTCAA
 TTACCTTTCTGTGGTCCTAATGTCATAGATCACTTTATGTGTGATCTCTACACTTTGATCAA
 TCTTGCTGCACTAATACCCACACTCTAGGACTCTTCATTGCTGCCAACAGTGGGTTCATAT
 GCCTGTAAACTGTCTCTTGCTCCTGGTCTCCTGCGTGGTCATACTGTACTCTTAAAGACC
 55 CACAGCTTAGAGGCAAGGCATGAAGCCCTCTCTACCTGTGTCTCCACATCACAGTTGTCA
 TCTTATCCTTTATACCCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDSHLHTPMYFFLCN
LSFLDVCYTSSSVPLILASFLAVKKKVSFSGCMVQMFISFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI
SINVISMGTGNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFSTCSAHLTVVIIFYGTIFFMYAKP
10 ESKASVDSGNEDIEALISLFYGVMTPLNPLIYSLRNKDVKAAVKNILCRKNFSDGK (SEQ ID
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTCTGCTAGGGCTTTCTGCCACC
CAAAGCTCCAGACAGTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGGA
15 AATGGAGTCCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCATGTATTTCTT
CCTCTGTAATCTTTCTTCTCGACGTTTGCTACACAAGTTCTCTGTCCCACTAATTCTTG
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTTCTCTGGGTGTATGGTGCAAAATGTTTAT
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGCTACCCACTGAGATACCCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA
20 TGCCAGCTGGGTCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT
GCAGTTACCATTCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTCTGGCTATCT
TGAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTCAATCTGAT
TGTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT
GAGGATTCCCTTCCACTGAAGGAAAAACATAAGGCCCTTCTCCACCTGCTCAGCCACCTGACA
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT
CTGTTGATTCAAGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYFLSNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTCQVIAAGSWMTGCLTAMVEMMSVLPLSLCGNSIINHFTCEILAILKLVCDTS
LVQLIMLVISVLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVILFYGTALSMH
35 LKPSAVDSQEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKLLIRNHFNTAFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTCTTCTGCGGATTTTTTCACTACCC
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC
40 AACATTTTCTGATCTCCATCACCATTCTAGATCCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCCTCTCTCCAATGCTGG
CAAACCTTTGTTTCAGGGAGAAACACTATTTTCACTTCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGATACCCTGTCATCATGAATAGGAGAACCTGTGTGCAGA
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAAATGATGTCTGTGCT
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTTTCACTTGTGAAATTCTGGCCATCT
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT
TCTTCTCCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCCTCGCCAGTATCC
TGAGAATCAGTTCAGTGGAAGGTCGAAGTAAAGCCTTTTCAACGTGCACAGCCACCTGA
50 TGGTGGTAGTTTGTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGATTA
GAAATCATTTTAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

AOLFR209 sequences:

- MDKINQTFVREFILLGLSGYPKLEIIFLILVMYVVLIGNGVLIASILDSRLHMPMYFFLGNLS
 FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLGMMAFDRYVAICNPLRY
 5 PIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNTV
 TLAVSNIAFLVPLLVIFFSYMFIYILRTNSATGRHKAFSTCSAHLTVVIIFYGTIFFMYAKPKS
 QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
 389)
- 10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC
 CCAAACCTTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
 AATGGTGTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT
 CCTGGGCAACCTCTCTTTCTGGATATCTGCTATACAACCTCCTCCATTCCCTCAACACTGG
 TGAGCTTAATCTCAAAGAAAAGAAACATTTCCTTCTCTGGATGTGCAGTGAGATGTTCTT
 15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCTCTTGGCATGATGGCATTGATCGTTAT
 GTGGCCATCTGTAACCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
 TGACTTCTGTATCATGGCTTTCTGGTGAATCAATTCAACTGTGCAAACATCACTTGCCAT
 GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTTCTTATGCGAGATCTTAGCTGTCC
 TAAATAAGCTTGTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAATATTGCT
 20 TTCCTAGTTCTTCTCTGCTCGTGATTTTTTCTCCTATATGTTTCATCCTCTACACCATCTTG
 CGAACGAACCTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG
 TGGTGATCATATTTATGGTACCATCTTCTTATGTATGCAAAACCTAAGTCCCAGGACCTC
 CTGGGAAAGACAACCTGCAAGCTACAGAGGGGCTTGTTCATGTTTATGGGGTTGTGA
 CCCCCATGTTAAACCCCATATCTATAGCTTGAGAAATAAAGATGTAAGCTGCTATAAA
 25 ATATTTGCTGAGCAGGAAAGCTATTAACCAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

- MMGRRNDTNVADFILTLGLSDSEEVQMALFMLFLLIYITMLGNVGMILLIIRLDLQLHTPMYFFL
 THLSFIDLSYSTVVTPKTLANLLTSNYISFTGCF AQMFCFVFLGTAECYLLSSMAYDRYAICSP
 30 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVVSMRSLHFCD SNIIHHFFCDTSPILALSCTDTDN
 TEMPLIFHAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTFYGTMIIFYLKP
 RKSYSLGRDQVAPVFYTTIVPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)
- 35 ATGATGGGTAGAAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
 TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT
 GGGGAATGTGGGGATGCTATTGATAATCCGCTGGACCTCCAGCTTCACACTCCCATGTAT
 TTTTCTTACTCACTGTCAATTTATTGACCTCAGTTACTCAACTGTCGTACACCTAAAAC
 CTTAGCGAACTTACTGACTTCCAATAATTTCTTACAGGGCTGCTTTGCCAGATGTTCT
 GTTTGTCTTCTTGGGTACTGCTGAATGTTATCTTCTCCTCAATGGCCTATGATCGCTAT
 40 GCAGCGATCTGCAGTCTCTACACTACACAGTTATTATGCCAAAAGGCTCTGCCTCGCTC
 TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC
 AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTCTGTGACACTTCCCCAATTTT
 AGCTCTGTCTGCACTGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTC
 ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTTACCATCCT
 45 GAAAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTACTTGGCTCTCATCTCTTG
 GGAGTCACCATCTTCTATGGAATATGATTTTACTTAAAGCCAAGAAAGTCTTATT
 CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTATACTATTGTGATTCCCATGCTGAATCC
 ACTATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
 AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)
- 50

AOLFR211 sequences:

- MMGRRNNTNVADFILMGLTLSEEIQMALFMLFLLIYITMLGNVGMILLIIRLDLQLHTPMYFFL
 THLSFIDLSYSTVVTPKTLANLLTSNYISFTGCF AQMFFFAFLGTAECYLLSSMAHRYAICSP
 LHYTVIMSKRLCLALITGPYVIGFIDSFVNVVSMRSLHFYDSNVIIHHFFCDTSPILALSCTDTYNT
 55 EILFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTFYSTLIFTYLPKPRK
 SYSYSLGRDQVASVFYTTIVPVLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)

ATGATGGGTAGAAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG
 5 GGGAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT
 TTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAACC
 TTAGCGAACTTACTGACTTCCAACCTATATTTCCCTTACGGGCTGCTTTGCCAGATGTTCTT
 TTTTGCCTTCTTGGGTACTGCTGAATGTTACCTTCTCTCCTCAATGGCCCATGATCGCTATG
 CAGCGATCTGCAGTCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT
 CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA
 10 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTTCTGTGACACTTCCCCAATTTTA
 GCTCTGTCTGCACTGATACATAACAACCCGAAATCCTGATATTCATTATTGTTGGTTCCAC
 CCTGATGGTGTCCCTTTTACAAATATCTGCATCCTATGTGTTCACTTCTTTACCATCCTGA
 AAATTAATTCACCTTCAGGAAAGCAGAAAGCTTCTCTACTTTCGCTCTCTCATCTCTTGGG
 AGTCACCATCTTTTATAGCACTCTGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCCT
 15 TGGGAAGAGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCGTGTGAATCCACT
 CATTTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCTCAGAGTCATGCAGAGAAG
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20 MAGNNFTEVTVFILSGFANHPQLVSLFLMFLFIYLFVVLGNLGLITLIRMDSQLHTPMYFFLSN
 LAFIDIFYSSTVTPKALVNFQSNRRSISFVGVQMYFFVGLVCCFCFLGSMAYNRYIAICNPL
 LYSVVMQKVSINWLGVMPIYVIGFTSSLSVWVISSLAFCDSSINHFFCDTTALLALSCVDTFGT
 EMVSFVLGFTLLSLLIITVYIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLPD
 NTSSLTQAQVASVFYTTVPMNLPLIYSLRNKDVKNALLRVIHRKLP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTTGCAAATCACC
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCATTTATCTATTCACTGTTTTGGGA
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTTT
 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG
 30 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTTCAAATGTACTT
 TTTTGTGATTGGTGTGTTGTGAGTGTTCCTTCTGGGATCAATGGCCTACAATCGCTACA
 TAGCAATCTGCAATCCCTTACTGTATTCACTAGTATGATGTCCAAAAAGTGTCCAATGGCT
 GGGAGTAATGCCATATGTGATAGGCTTCACAAGCTCGTGATATCTGTCTGGGTGATAAGC
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTTGTGACACCACAGCTTTTTAGC
 35 ACTCTCTGTGTAGATACATTCCGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT
 CTTCTTAGCTCTCTCCTTATCATCACAGTCACTTATATCATCATCATCTCAGCCATCCTGAG
 GATCCAGTCAGCAGCAGGCAGGCAGAAAGGCCTTCTCCACCTGCGCATCCCACCTCATGGCT
 GTAACATATCTTTATGGGTCTCTGATTTTACCTATTTGCAACCTGATAACACATCATCGCT
 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTCAATCCCATGCTGAATCCACTC
 40 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA
 CTTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45 MNSLGKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDIFILLGFSDBPRL
 EAVLFVFFVLFYLLTLVGNFTIIISYLDPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLASISWLSGLA
 SSLIHATFTLQLPLCGNHRLDHFICEVPALLKLACVDTTVNELVLFVSVLFPVIPPALISISYGF
 TQAVLRIKSVEARHKAFSTCSSHLTVVHIFGTIIYVYLQPSDSYAQDQGFISLFYTMVPTLNP
 IYTLRNKMDKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA
 ATTTAATTGTTTTGGATGTACCCATTCCATTCCCTGCCTTAGGTGCGGATCCCCCTGGAGGG
 ATGGGATTGGGCAATGAGAGTTCCCTAATGGATTTTCATCCTTCTAGGCTTCTCAGACCACC
 CTCGTCTGGAGGCTGTTCTCTTTGTATTGTCTTTTCTTCTACCTCCTGACCTTGTGGGA
 55 AACTTCACCAATAATCATCATCTCATATCTGGATCCCCCTTTCATACCCCAATGTACTTTTT
 TCTCAGCAACCTCTCTTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCCTAATCCATGCAACTTTTACCTTG
 5 CAATTGCCTCTCTGTGGCAACCATAGGCTGGACCATTTTATTTGCGAAGTACCAGCTCTTCT
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGGTGGCTTTTGTGTAGTGTCTGT
 TTGTGTGTCATTCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCACCTTACAG
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAACTTCTCTCGGGA
 AAATTGTGA (SEQ ID NO: 398)

AOLFR214 sequences:

15 MDKSNSSVSEFVLLGLCSSQKLQLFYCFFSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN
 LSFVDICQASFATPKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY
 YVVMISRRCTCTVLMISWAVSLVHTLSQLSFTVNLPFCGPNVDSFFCDLPRVTKLACLDSEYIE
 ILIVVNSGILSLSTFSLVSSYIILVTVWLKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS
 20 PLDKFLAIFYTVFTPVLPNIYTLNRNMDKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID
 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTACTGTTGGGACTCTGTAGTTCTC
 AAAAAGTCCAGCTTTTCTATTTTGTCTTCTCTGTGTTGTATACAGTCATTGTGCTGGGA
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCCTATGTACTTTCT
 25 CTGGGAAACCTTTCCCTTTGTGACATTTGTTCAGGCTTCTTTGTCTACCCCTAAAATGATTG
 CAGATTTTCTGAGTGCACACGAGACCATATCTTTTCAGTGGCTGCATAGCCCAAATTTTCTTT
 ATTCACCTTTTACTGGAGGGGAGATGGTGTCTACTTGTTCGATGGCCTATGACAGGTATG
 TAGCCATATGCAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGCACACATTAAGCCAGTTATCATTACTGTG
 30 AACCTGCCCTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTGTGATCTTCTCGAGTCAC
 CAACTTGCCTGCCCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAATT
 CTTTCCCTAAGCACTTTCTCTCTCTTGGTCAGCTCCTACATCATTATCTTGTACAGTTTG
 GCTCAAGTCTTCAGCTGCAATGGCAAAGGCATTTCTACGCTGGCTTCCCATATTGCAGTA
 GTAATATTATCTTTGGACCTTGCATCTTCATCTATGTGTGGCCCTTTACCATCTCTCCTTT
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTTCACCCCCGTCCTAAACCCATTATTTATA
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATTACCTGAGGC
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA (SEQ ID NO:
 400)

AOLFR215 sequences:

40 MAHTNESMVSEFVLLGLSNWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNSPMYFLLSNL
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH
 YSTIMNRRLCVIFVSISWAVGVLHVSFLAFTVDLPFCGPNEVDSFFCDLPLVIELACMDTYEM
 EIMTLTNSGLISLSCFLALHSYTHLIGVRCRSSSGSSKALSTLTAHITVVILFFGPCIFYFWPFSRL
 45 PVDKFLSVFYTVCTPLNPIYSLRNEDVKAAMWKLNRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT
 GGGGACTTCAACTTTTCTTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC
 AATGTCTTAATTATTGTCATTATTTCTTTTGTACTCCCATTTGAACTCTCCTATGTACTTCTTG
 50 CTCAGTAATCTTTCTTTCATTGATATCTGTCACTAAGTCTAAGTCTGCACTGCTGCTGCTG
 AGACTTTTATTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCAGATATTCGTT
 CTTACAGTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT
 TGTGTCTATTTCTGGGCGGTGGGCGTTCTTCATTCTGTGAGCCACTTGGCTTTTACAGTGG
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG
 ATGCAGGTCCTCCAGTGGGTCATCTAAGGCTCTTTCTACATTAAGTGGCCACATCACAGTG
 GTCATTCTTTTCTTCGGGCTTGCATTTATTTCTATATATGGCCTTTTAGCAGACTTCCTGT
 GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTGAACCCCATCATCTACT
 5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAACT
 CCTGGAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNLIVITVIVDPHLHSPMYFLL
 10 TNLSIIDMSLASFATPKMITDYLTHGKHTISFDGCLTQIFLHLFTGTEILLMAMSFDRYIAICKPL
 HYASVISPVQVCVALVVASWIMGVMHMSMSQVIFALTLPFCGPYEVDSSFFCDLPVVFQLACVDTY
 VLGFLMISTSGIILSCFIVLFNSYVTVLVTVKHSSRGSSKALSTCTAHFIVVFLFFGPCIFIYMW
 PLSSFLTDKILSVFYTIFTPTLNPITYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTGTTTTGCTGGGGCTCTCTAATTCCT
 GGGAACACAGATGTTTTCTTTATGGTGTTTTCAATGCTTTATGTGGCAACAATGGTGGG
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC
 TGCTTACCAATCTTCAATCATTGATATGTCTCTTGCTTCTTTCGCCACCCCAAGATGATT
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTGATGGCTGCCTTACCCAGATATTCT
 20 TTCTCCACCTTTTCACTGGAACCTGAGATCATCTTACTCATGGCCATGTCTTTGATAGGTAT
 ATTGCAATATGCAAGCCCCTGCACTATGCTTCTGTCTATTAGTCCCCAGGTGTGTGTTGCTCT
 CGTGGTGGCTTCCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC
 ACGTTACCATCTGTGGTCCCTATGAGGTAGACAGCTTTTCTGTGACCTTCCTGTGGTGTT
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCTCTTATGATCTCAACAAGTGGCATA
 25 ATTGCGTTGTCCTGTTTTATTGTTTTATTAAATTCATATGTTATTGTCCTGGTTACTGTGAA
 GCATCATTCTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTTCATTGTTG
 TCTTCTTGTCTTTGGGCCATGCATCTTCATCTACATGTGGCCACTAAGCAGCTTTCTCACA
 GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCCAATAATCTATAC
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAAACTGAAAAATAGGTTTCTAAATTT
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAI SFEGCMTQMFFLHLLGGAEIVLLISMSFD
 35 RYVAICKPLHYLTIMSRRCVGLVILSWIVGIFHALSQAFTVNLFPFCGPNEVDSSFFCDLPLVIK
 LACVDTYILGVFMISTSGMIALVCFILLVISYTIILVTVRQRSSGSSKALSTCSAHFTVVTLFFGP
 CTFIYVWPFTNFPIDKVLVSVFYTYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRLTDHTP
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
 GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCCTGTTTTT
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTGCATCA
 GAGCCACACCTTCATTCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC
 CCTGGCCTCATTGCCCACCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGTGAGATTG
 TACTGCTGATCTCCATGTCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTCTCGGATTGTGCGGCATCT
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT
 AGACAGTTTCTTTTGTGACCTCCCTTTGGTGATTAAACTTGCTTGTGTGACACATATATTC
 50 TGGGGTGTTCATGATCTCAACCAAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTTGGT
 GATCTCTTACACTATCATCCTGGTCACCGTTCGGCAGCGTTCCTCTGGTGGATCCTCCAAA
 GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCTTTTCTTTGGCCCATGCATTT
 CATTTATGTGTGGCCTTTACAAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
 TATACACTCCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC
 55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA
 (SEQ ID NO: 406)

AOLFR218 sequences:

METANYTKVTEFVLTGLSQTREVQLVLFVIFLSFYLFILPGNLIICTIRLDPHLTSPMYFLLANLA
 LLDIWYSSITAPKMLIDFFVERKIISFGGCCIAQLFFLHFVGASEMFLIVMAYDRYAICRPLHYA
 5 TIMNRRLLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
 ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVLMMFGPSIYTYARPF
 SFSLDKVVSVFHTVIFLLNPIIYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
 10 GGGAGGTCCAACTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
 AATATCCTTATCATTTGCACCATCAGGCTAGACCCTCATCTGACTTCTCCTATGTATTTCCCT
 GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTTCCATTACAGCCCCTAAAATGCTCA
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT
 CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT
 15 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGTCTCTGCTGTATCCT
 GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCACTCTATAATACAGGTGGCTCTCATTGTT
 CGACTTCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTG
 TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT
 GATCTCTGTGGTGTGTTTCATTGCTCTGTTAATGTCCTATGCCTTCTTCTGGCCTGTCTCA
 20 AGAAACATTACAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCACAT
 TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT
 TTTCCCTAGATAAAGTGGTGTCTGTGTTTCATACTGTAATATTCCTTTACTTAATCCCATT
 ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT
 ATTTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

AOLFR219 sequences:

MLTSLTDLCFSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLFTFSLLYLAILLGNF
 LILTVTSDSRHLTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS
 EMVLLVSMAYDRYVAICKPLHYMTVMSRRVCVVLVLISWVFGFIHTTSQLAFTVNLPCGPN
 30 KVDSEFFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVSYSYTVILVTVRNRSSASMAKAR
 STLTAHITVVTLFFGPCIFIYVWPFSYSVDKVLAVFYTIFTLLNPVIYTLRNKEVKAAMSKLKS
 RYLKPSQVSVVIRNVLFLETK (SEQ ID NO: 409).

ATGCTCACTTCATTAACCTGATCTCTGTTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT
 35 TCCAAAATCGATGAATGAGACAAATCATTTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG
 TCTAGTTCAAGGGAGCTCCAACCTTTCTGTTTCTTACATTTTCACTACTTTATCTAGCAAT
 TCTGTTGGGCAACTTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA
 TGTACTTTCTGCTTGCAAACCTGTCATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT
 AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC
 40 AGATTTTCTTTGTTTCATCTCTTCACTGGCAGTGAATGGTGCTCCTAGTTTCCATGGCCTAT
 GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT
 GTGTTGTGCTCGTCCTCATTTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA
 TTCACTGTTAATCTGCCATTTTGTGGTCCTAATAAGGTAGACAGTTTTTTCTGTGACCTTCC
 TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTGACGTTACTAATAGTTGCAGAT
 45 AGTGGCTTTCTTCTCTGAGTTCTTTCTCCTCTTGGTTGTCTCCTACACTGTAATACTTGT
 ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA
 TCACTGTGGTCACTTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT
 TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCCTGT
 AATCTACACGCTAAGAAACAAGAGTGAAGGCAGCTATGTCAAAACTGAAGAGTCGGTA
 50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTAGAAACAAAGTAA
 (SEQ ID NO: 410).

AOLFR220 sequences:

MKQYSVGNQHSNYRSLLPFLCSQMTQLTASGNQTMVTEFLFSMFPHAHRGGLLFFIPLLLIYG
 55 FILTGNLIMFIVIQVGMLHTPLYFFISVLSFLEICYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF
 HSLGITESCVLTAAMDRYIAICNPLRYPTIMIPKLCIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIIIVILGMHSAEGHHKAFST
CAAH LAVFLFFGSVAVMYLRF SATYSVFWDTAIAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTTCCTTTTCT
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCCTTGCTTCTCA
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTTCATTGTCATCCAGGTGGGCATGGC
CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCCTTCCTGGAGATCTGCTATACCA
10 CAACCACCATCCCCAAGATGCTGTCTGCCTAATCAGTGAGCAGAAGAGCATTTCGGTGGC
TGGCTGCCTCCTGCAGATGTACTTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCTG
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCTCCTTG
CTTCTGAGATTGCATGGATTTCCACCTTGCTTTCTGTGGCTCCAACCAGATCCACCAGAT
15 ATTCTGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCTAGTGGTCATT
GTGGATGCCATCCATGCAGCGGAAATTGTAGCCTCCTTCCTGGTCATTGCTCTATCCTACA
TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAGGCCCTTTTC
CACCTGTGCTGCTCACCTTGCTGTGTTCTTGCTATTTTTTGGCAGTGTGGCTGTCTGTATT
TGAGATTCTCAGCCACCTACTCAGTGTTTTGGGACACAGCAATTGCTGTCACTTTTGTATC
20 CTGCTCCCTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

25 MRNLSGGHVEEFVLVGFPTTPPLQLLLFVLFVFFAIYLLTLENALIVFTIWLAPSLHRPMYFFLGH
LSFLELWYINVTIPRLAAFLTQDGRVS YVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP
LLYPSLMPSSLATRLAAASWGS GFSSMMKLLFISQLSYCGPNIINHFFCDISPLNLTCS DKEQA
ELVD FLLALVMILLPLLAVVSSYTAIIAILRIPTSRGRHKAFSTCAAH LAVVVIYSS TLFTYAR
PRAMYTFNHNKIISVLVYTIIVFFNPAIYCLRNKEVKEAFRK TVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

ATGAGAAATTTGAGTGGAGGCCATGTCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
CTCCCTCCAGCTGCTCCTCTTTGTCTTTTGTGCAATTTACCTTCTGACATTGTTGGAGA
ATGCACTTATTGTCTTACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATTGACTTTTTT
35 CTGGCCATCTCTCTTTCCCTGGAGCTATGGTACATCAATGTCAACATTCTCGGCTCTTGGC
AGCCTTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACTGTACTTC
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT
GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTATTTCCCAA
40 TTGTCTACTGTGGACCCAAACATTATCAACCACTTTTTCTGTGATATTTCCCACTACTCAA
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACACTGCCATCATTGCAGCCATCCTGAG
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
GTTGTTATCTACTACTCCTCCACTCTCTTCACCTATGCACGGCCCCGGGCCATGTACACCTT
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT
GTCATATCCTAGGGATGTTCAAGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLT SNVFIHAIRLDSHLHTPMYFLSFL
SFSETCYTLGIIPRMLSGLAGGDQAISYVGAAQMFFSASWACTNCFLLAAMGFDRYVAICAPL
HYASHMNPTLCAQLVITSFLTGYLFGLGMLTVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS
ELRIFILSLLVLLVSFFITISYAYILAILRIPSAEGQKKAFTSCASHLTVVIIHYGCASFVYLRPK
ASYSLERDQLIAMTYTVVTPLLNPIVYS LRTRAIQTALRNAFRGRLLGK (SEQ ID NO: 415).

55

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTTGTCTTCCTGGGCTTCTCCAGTTCTG
 GGGAGTTGCAGCTCCTTCTCTTTGCCTTGTTCCTCTCTCTGTATCTAGTCACTCTGACCAGC
 AATGTCCTTCAATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCCATGTACCTCTT
 CCTTTCCTTCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCAGATGTTCTT
 TTCTGCCTCATGGGCCTGTACTAACTGCTTCCTTCTGGCTGCCATGGGCTTTGACAGATATG
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCAGCT
 GGTCATTACTTCCTTCCTGACTGGATACCTCTTTGGACTGGGAATGACACTAGTTATTTTC
 ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG
 10 AGCCTAGCCTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTGG
 TCCTCTTGGTCTCCTTCTTCTTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG
 AGGATCCCCTCTGCTGAGGGGCAGAAAGAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG
 TGGTCATTATTATTATGGCTGTGCTTCCTTCGTGTACCTGAGGCCCAAAGCCAGCTACTCT
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

MEAANESSEGISFVLLGLTSPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
 20 HLSFADLCFASVTVPKMLANLLAHDHSISLAGCLTQMYFFALGVTDSCLLAAMAYDCYVAIR
 HPLPYATRMSRAMCAALVGMALVSHVHSLLYILLMARLSFCASHQVPHFFCDHQPLLRLSC
 SDTHHIQLLIFTEGAADVVPFLILASYGALAAAVLQLPSASGRLRAVSTCGSHLAVVSLFYGT
 VIAVYFQATSREAEWGRVATVMYTVVTPMLNPIIYSLWNRDVQGALRALLIGRRISASDS
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTTCGTTTTATTGGGACTGACAACAA
 GTCCTGGACAGCAGCGGCCTCTCTTTGTGCTGTTCTTGCTCTTGTATGTGGCCAGCCTCCTG
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT
 TCCTGCTGGCCACCTGTCTTTGCTGACCTCTGTTTCGCCTCCGTCAGTGTGCCAAAGATG
 30 TTGGCCAACTTGTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT
 ACTTCTTCTTTGCCCTGGGGGTAAGTATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG
 CTACGTGGCCATCCGGCACCCCTCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA
 GCCCTGGTGGGAATGGCATGGCTGGTGTCCACGTCCACTCCCTCCTGTATATCCTGCTCA
 TGGCTCGCTTGTCTTCTGTGCTTCCCAACAAAGTGCCCACTTCTTCTGTGACCACAGCCT
 35 CTCTTAAGGCTCTCGTGCTCTGACACCCACCACATCCAGCTGCTCATCTTACCGAGGGCG
 CCGCAGTGGTGGTCACTCCCTTCTGCTCATCTCGCCTCCTATGGGGCCATCGCAGCTGC
 CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCCAC
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCACTACTTCCAGGCCACATCCC
 GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTCATGTACACTGTAGTACCCCCATGC
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGCACTCCGAGCCCTTCT
 CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

MGSFNTSFEDGFILVGFSDWPQLEPILFVFIFYSITLFGNTIIIALSWLDLRLHTPMYFFLSHL
 45 LDLCFTTSTVPQLLINLCGVDRITTRGGCVAQLFIYLALGSTECVLLVVMMAFDRYAAVCRPLHY
 MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT
 EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTCSHLLVFLFYGSAITYT
 YLQSIHNYSEREGKFVALFYTIITPILNPLYTLRKNKDVKGALWKVLWRGRDSG (SEQ ID NO:
 419).

50 ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC
 CGCAACTGGAGCCCATCCTGTTTGTCTTTATTTTATTTTCTACTCCCTAACTCTCTTTGGC
 AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTCAACACCAGCACCGTGCCCCAGCTCCTGA
 55 TCAACCTTTGCGGGGTGGACCGCACCATACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGATGGCCTTTGACCGCTAT

GCTGCTGTCTGTCGTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT
 GGCTATCGCCTCCTGGGGTGCGGGTTTCGTGAACTCTCTGATCCAGACAGGTCTCGCAATG
 GCCATGCCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA
 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCCGAGTCATAGT
 5 CGTGGCTGTTCCCTGCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
 AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA
 GTAGTTTTCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC
 TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTTATACTATAATTACCCCCATTCTCAATCCTC
 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG
 10 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

MENYNQSTDFILLGLFPPSIIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
 LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLSMAYDRYIAICFPLHYLIRM
 15 SKRVCVLMITGWSWIGSINACAHTVYVLHIPYCRSRRAINHHFCDVPAMVTLACMDTWVYEGTV
 FLSATIFLVFPFIGISCSYGQVLFAVYHMKSAEGRKKAYLTCSTHLTVVTFYYAPFVYTYLRPRS
 LRSPTEDKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCATCAA
 20 TAATTGACCTTTTCTTCTTCACTTCTATTGTTTTCATTTTCTGATGGCTCTAATTGGAAACC
 TGTCCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCCCTACTG
 AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATTTGTTCCCTAAGATGGCATCTGA
 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTGAGAGTTTCTTCTTCT
 TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC
 25 TATTTGCTTTCTCTCCACTATCTCATCCGCATGAGCAAAAAGAGTGTGTGTGCTGATGATA
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA
 TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCCAGCAATGGTGACT
 CTGGCCTGCATGGACACCTGGGTCTATGAGGGCACAGTGTTTTTGAGTGCCACCATCTTTC
 TCGTGTTCCTTTCATTGGTATTTTCATGTTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC
 30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA
 GTAACCTTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC
 AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCCTCACCCCAATGCTCAACCCCATC
 ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC
 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

35

AOLFR226 sequences:

MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLLAYVLVLTENTLIIMAIRNHSTLHKPMYFFL
 ANMSFLEIYWYVTVTIPKMLAGFVVGSKQDHGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
 RYMAICYPLHYPVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNIINHFFCDVSPLL
 40 NLSCTDMSTAELTDFILAFILLGPLSVTGASYVAITGAVMHISAAAGRYKAFSTCASHLTVVIIF
 YAASIFIYARPKALSAFD TNKLVSVLYAVTVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP
 KKASRNV (SEQ ID NO: 423).

ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT
 45 CCTGCGCCACTACAGGTACTATTGTTTGCCCTTTTGTGCTGCTGGCCTATGTGTTGGTGCTGAC
 TGAGAACACACTCATCATTATGGCAATTAGGAACCATCTACCCTCCACAAACCATGTAC
 TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
 GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC
 ATGACACAGCTCTACTTTTCTTGGCTTGGGCTGCACTGAGTGTGTCCTTCTCGCTGTTAT
 50 GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCACTGGCC
 GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTGGCATCTCCATGGTCAA
 AGTTTCTTATTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTCTGTG
 ATGTCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTT
 ATCCTGGCCATTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT
 55 TACTGGTGCTGTGATGCACATATCTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT
 GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTA
CCATTGCTCAATCCCATCATTTACTGCCGTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

5

AOLFR227 sequences:

MEPQNTSTVTNLFQNLLEWQALLFVIFLLIYCLTIIGNVVITTVVSQGLRLHSPMYMFLQH
LSFLEVWYTSITVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
LRYPFLMHRGLCARLVVSVSWCTGVSTGFLHSMMSRLDFCGRNQINHHFFCDLPPLMLQLSCSRV
YITEVTIFILSIAVLCICFFLTGPLYVFIVSSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMVY
CPSPHLLPEINKIISVFYTVVTPLLNPVYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF
LY (SEQ ID NO: 425).

10

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTTCAGCTGTAGGATTCCAGAACCTTC
TTGAATGGCAGGCCCTGCTCTTTGTCAATTTCTGCTCATCTACTGCCGTGACCATTATAGGG
AATGTTGTCATCATCACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCCTATGTACATGT
TCCTCCAGCATCTCTCCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCTTCTCCTA
GCCAACCTGCTGTCTGCGGGCCAAGCCATCTCCTTCTCTGCTGCATGGCAGCCTACT
TCTTCGTATTCTCGCGGCCACCGAGTGCTTTCTCCTGGCCTTCATGGCCTATGACCGTTAC
CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT
GGTGGTGGTCTCATGGTGCACAGGGGTCAGCACAGGCTTTCTGCATTCCATGATGATTTCC
AGGTTGGACTTCTGTGGGCGCAATCAGATTAAACCATTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC
GTGCTGTGCATTTGTTTTTTCTGACACTGGGGCCCTATGTTTTTCATTGTGTCTCCATATT
GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCACCTGGCT
GTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCCAGTCCCCACCTGTT
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTCAACCACTGCTGAACCCA
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG
AAATGTGGTATTCTATGGAGTACAAGTAAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

30

AOLFR229 sequences:

MFYVNQIPFQLYHISFVYPTLWSRAIIPCMTLSFWVCSATPVSPGFFALILLVFTVSIASNVVK
IILIHDSRLHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE
FFLLGLMSCDRYVAICNPLHYPDLMSRKICWLIVAAAWLGGSIDGFLLPVTMQPFPCASREIN
HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFVSISGSYTRILITVYRMSEAEGRRKAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQK
VVGRVCVSSGKVTF (SEQ ID NO: 427).

35

ATGTTTTATGTAAATCAGATACCTTTCCAACCTTTATCATATCTCTTTCGTGTACCCTACAGA
GCTATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA
ACGCCCCGTTTCCCCTGGCTTCTTTGCCCTCATTCTCCTGGTCTTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTC
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCT
GGTCGACCAGGTGATGAGCCAGAGAGCCATTTCCCTTGTCTGGATGCACTGCCCAACACTTC
CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTTAGGACTCATGTCTGTGATCGCTA
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTACCA
TGCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTA
TGATGCTCCTCATCCCTTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG
GTGGTTGTGACCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
CACCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT
CCACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGGCCCTACAGAAGGTTGTTGGG
AGGTGTGTGCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

55

AOLFR230 sequences:

MGMEGLLQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMD SRLHTPMYFLLS
 QLSIMDTTYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTLIGGEFFLLGLMAYDRYVAVCNP
 LRYPLLNNRRVCLFMVVGSWVGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKLSDTDS
 5 LYETLMYACCVLMLLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVSIFYGAIFY
 TNVLPHSYHTPEKDKVVSIFYTILTPMLNPLIYSLRNKDVAAALRKVLGRCGSSQSIRVATVIR
 KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCTCACAGGCCTCATCACCC
 10 ATCTGCCTTCCCCGGGCTTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA
 GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCTCCACACACCCATGTACTT
 CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC
 TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCTTCTGGGCTGTGCAGTTCAGATCTT
 CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCTGCTGGGTCTCATGGCCTATGACCGC
 15 TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT
 CATGGTGGTCGGCTCCTGGGTTGGTGGTTCCTTGGATGGGTTCATGCTGACTCCTGTCACT
 ATGAGTTTCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCAGCCGT
 GCTGAAGTTGTCTTGACAGACACGTCACCTCTATGAGACCCTGATGTATGCCTGCTGCGTG
 CTGATGCTGCTTATCCCTCTATCTGTCATCTGTCTCCTACACGCACATCCTCCTGACTGT
 20 CCACAGGATGAACCTGCTGAGGGCCGGCGCAAAGCCTTTGCTACGTGTTCTCCACATT
 ATGGTGGTGAGCGTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC
 AACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTCACCCTCATGCTCAA
 CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG
 GAGATGTGGTTCCTCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
 25 NO: 430).

AOLFR231 sequences:

MERANHSVSVSEFILLGLSKSQNLQILFFLGFSVVFVGIVLGNLLILVTVTDSLHTPMYFLLSNL
 SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMAIDRYVAICKP
 30 LHYMTIMSPRVLTGILLSSYAVGVFVHSSQMAFMLTLPFCGPNVIDSFFCDLPLVIKLACKDTYI
 LQLLVIADSGLLSLVCFLLLVSYGVIFSVRYRAASRSSKAFSTLSAHITVVTLFFAPCVFIYVW
 PFSRYSVDKILSVFYTIFTPLNPIIYTLRNQEVKAAIKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATTCAGTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC
 35 AAAATCTTCAGATTTTATCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA
 AACCTGCTCATCTTGGTGACTGTGACCTTTGATTGCTCCTTCACACACCAATGTATTTCT
 GCTTAGCAAACCTCTCCTGCAATTGATATGATCCTGGCTTCTTTTGCTACCCCTAAGATGATTG
 TAGATTTCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATTCCAGATGTTCTT
 TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT
 40 GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC
 TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTTCATGTTG
 ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTCTGTGACCTTCCCTTGTGAT
 TAAACTTGCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC
 CTGTCACTGGTCTGCTTCTCTCTTGTCTCTCTATGGAGTCATAATATTCTCAGTTAG
 45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTTCTCCACTCTCTCAGCTCACATCACAGTTG
 TGACTCTGTTCTTTGCTCCGTGTGTCTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA
 GATAAAATCTTTCTGTGTTTACACAATTTTCACACCTCTCTAAATCCTATTATTTATAC
 ATTAAGAAATCAAGAGGTAAAAGCAGCCATTAAGAAAGACTCTGCATATAA (SEQ ID NO:
 432).

50

AOLFR232 sequences:

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
 VIFVFLMALSGNAVILLIHCD AHLHTPMYFFISQLSLMDMAYISVTVPKMLLDQVMGVNKIS
 APEGCMQMFFYVTLAGSEFFLATMAYDRYVAICHPLRYPVLMNHRVCLFSSGCWFLGSVD
 55 GFTFTPTMTFPFRGSREIHFFCEVPAVLNLSGSDTSLYEIFMYLCCVLMMLIPVVISSSYLLILL

TIHGMNSAEGRKKAFAATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDDMMVSVFYTILTPVVNP
LIYSLRNKDVGMALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTTCATCCTGATGGGAC
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCTGATCCTTCTGATACA
CTGTGACGCCCACCTCCACACCCCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACA
TGGCGTACATTTCTGTCACTGTGCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAA
10 GATCTCAGCCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTTCAGAA
TTTTTCTTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA
CCCTGTCTCATGAACCATAGGGTGTGTCTTCTCTGTCATCAGGCTGCTGGTTCCTGGGCT
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCGGGA
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC
15 TCTATGAGATTTTCATGTACTTGTGCTGTGTCTCATGCTCCTCATCCCTGTGGTGATCATT
TCAAGCTCCTATTTACTCATCCTCCTCACCATCCACGGGATGAACTCAGCAGAGGGCCGGA
AAAAGGCCTTTGCCACCTGCTCCTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCC
ATCTACACCTACATGCTCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG
TCTTCTATACCATCCTCACTCCAGTGGTGAACCTTTAATCTATAGTCTTAGGAATAAGGAT
20 GTCATGGGGGCTCTGAAGAAAATGTTAACAGTGAACCTGCCTTTCAAAAAGCTATGGAG
TAG (SEQ ID NO: 434).

AOLFR233 sequences:

25 MANITRMANHTGKLDFFILMGLFRRSKHPALLSVVIFVFLKALSGNAVLLILLHCD AHLHSPMY
FFISQLSLMDMAYISVTVPKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLLATMAYDR
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSVDGFMLTPITMSFPFCRSWEIHHFFCEVPAVTI
LSCSDTSLYETLMYLCCVLMLLIPVTIHSYLLILLTVHRMNSAEGRKKAFAATCSSHLTVVILFY
GAAVYTYMLPSSYHTPEKDDMMVSVFYTILTPVLNPLIYSLRNKDVGMALKKMLTVRFVL
(SEQ ID NO: 435).

30 ATGGCCAACATCACCAGGATGGCCAACCACACTGGAAAGTTGGATTTTCATCCTCATGGGAC
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCTGAAG
GCGTTGTCTGGAAATGCTGTCTGATCCTTCTGATACACTGTGACGCCCACCTCCACAGCC
CCATGTACTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG
35 CCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAAGGTCTCAGCCCCTGAGTGTGGG
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTCCGAATTTTCTTCTAGCCACCATGGC
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCCTCATGAACCATAGG
GTCTGTCTTTTCTGGCATCGGGCTGCTGGTTCCTGGGCTCAGTGGATGGCTTCATGCTCAC
TCCCATCACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG
40 TCCCTGCTGTAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCTCATGTACCTA
TGCTGTGTCTCATGCTCCTCATCCCTGTGACGATCATTTCAAGCTCCTATTTACTCATCCT
CCTCACCGTCCACAGGATGAACTCAGCAGAGGGCCGGA AAAAGGCCTTTGCCACCTGCTC
CTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC
45 GGTGCTGAACCTTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA
ATGTTAACTGTGAGATTCGTCCTTTAG (SEQ ID NO: 436).

AOLFR234 sequences:

50 MPNSTTVMEFLLMRFSVDVWTLQILHSASFFMLYLVTLMGNILIVTVTCDSSLHMPMYFFLRN
LSILDACYISVTVPTSCVNSLLDSTISKAGCVAQVFLVVFVYVELLFLTIMAHDYVAVCQPL
HYPVIVNSRICIQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLKLSGSDTFSNE
VMIVVSALGVGGGCFIIRSYIHIFSTVLGFPFGADRTKAFSTCIPHILVVSVFLSSCSSVYLRRP
AIPAATQDLILSGFYSIMPPLFNPIIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).

55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC
TACAGATTTTACATTCTGCATCCTTCTTATGTTGTATTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT
 CCCTACTGGACAGCACCACCATTTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT
 TTTTGTATATGTGGAGCTTCTGTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
 5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT
 GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
 CCCTTCTGTGCGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT
 CTCTTGCTCTGACACCTTCAGCAATGAGGTGATGATTGTTGTCTCTGCTCTGGGGGTAGGT
 GGCGGCTGTTTCATCTTTATCATCAGGTCTTACATTACATCTTTTCGACCGTGCTCGGGTT
 10 TCCAAGAGGAGCAGACAGAAACAAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG
 TCAGTCTTCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC
 CCAGGATCTGATCCTTTCTGGTTTTTATCCATAATGCCTCCCCTCTTAACCTATTATTTA
 CAGTCTTAGAAAATAAGCAAATAAAGGTGCCATCAAGAAAATCATGAAGAGAATTTTTTA
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

AOLFR235 sequences:

MDGVNDSSLQGFVLMGISDHPQLEMIFFIALLFSYLLTLLGNSTIILSRLEARLHTPMYFFLSNL
 SSLDLAFATSSVPQMLINLWGPKTISYGGCITQLYVFLWLGATECILLVMAFDRYVAVCRPL
 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
 20 NQAVLNGVCTFFTAVPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVVFYGSASYGY
 LLPAKNSKQDQGFISLFSYLVTPMVNPLIYTLRNMEVKALRRLGKGREVG (SEQ ID NO:
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
 25 CCCAGCTGGAGATGATCTTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCCTACTTGGG
 AACTCAACCATCATCTTGCTTTCCCGCCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT
 CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTCGCTACTAGTTCAGTCCCCCAAATGCTGA
 TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT
 CTTCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC
 30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCAAGCTCTGCTGGCTGC
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACTCT
 GCAGCTCCCAATTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCTGCCAT
 GATCAAACCTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT
 GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC
 AGCAAACAGGACCAGGGCAAGTTCATTTCCCTGTTCTACTCGTTGGTCAACCCATGGTGA
 ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

AOLFR236 sequences:

MTSQERDTAIYSINVSFVAKGMTSRSVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
 LFLLIYSITVAGNLLLLTVGSDSHLSLPMYHFLGHLSFLDACLSTVTVPKVMAGLLTLDGKVIS
 FEBCAVQLYCFHFLASTEFLYTVMAYDRYLAICQPLHYPVAMNRRMCAEMAGITWAIGATH
 45 AAHTSLTFRLLYCGPCHIAFFCDIPPVLKLACTDITINELVMLASIGIVAAGCLILIVISYIFIVA
 AVLRIATAQGRQRAFSPCTAQLTGVLLEYVPPVCIYQPRSEAGAGAPAVFYTIVTPMLNPFYI
 TLRNKEVKHALQRLCSSFRESTAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCATTAATGTCAAGTTTGTGTGCAAAGG
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA
 CTGTGGTGAGCCACTTCTTCTGGAGGGTTTGAGGTACACCGCTAAACATTCTAGCCTCTT
 CTTCTCCTCTTCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCCTAA
 CTGTGGGCTCTGACTCTCACCTCAGCTTACCCATGTACCACTTCTGGGGCACCTCTCCTTC
 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTGATGGCAGGCCTGCTGACTCTGG
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
 TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT
 GTGGGCCCTTGCCACATTGCCTACTTCTTCTGCGACATACCCCTGTCTAAAGCTCGCCTGT
 ACAGACACCACCATTAAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT
 5 GCCTCATCCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
 GCCAGGGCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT
 ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC
 CCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCAATTTACACTTTGCGGA
 ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG
 10 CAGGCAGCCCACCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

MDQRNYTRVKEFTFLGITQSRELSQVLFITFLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL
 RNLSILDICFSSITAPKVLIDLSETKTISFSGCVTQMFFFHLLGGADVFLSVMAFDRIAISKPL
 15 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCNPNVLDTFYCDVPQVLKLACTDTFT
 LELLMISNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVTVLHFVPCIVVYA
 RPFTALPTDTAISVTFTVISPLLNPIIYTLRNQEMKLMRKLKRRLLQSERILIQ (SEQ ID NO:
 443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC
 GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACCTCTAATGGG
 AAATTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC
 TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCCTG
 ATAGATCTTCTATCAGAGACAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT
 25 TCTTCCACCTTCTGGGGGGAGCAGACGTTTTTCTCTCTGTGATGGCGTTTGACCGCTAT
 ATAGCCATCTCCAAGCCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
 TCATCGTGGGCTTCCTGGGTGGGGGGCTTGTCCACTCCATAGCGCAGATTTCTCTATTGCT
 CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCC
 TCAAACCTGCCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT
 30 AGTCAGTTGGTTTGTATTCTTCTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA
 GGTCTCACACTGGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACCG
 TGGTGACCCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCCGCCCTTCACTGCCCTCCCC
 ACAGACACTGCCATCTCTGTACACCTTCACTGTCACTCTCCCTTTGCTCAATCCTATAATTTA
 CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAACTGAAGAGACGGCTAGGAC
 35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

MAPENFTRVTEFILTGVSCEPQLIPLFLVFLVLYVLTMAGNLGIITLTSVDSRLQTPMYFFLRHL
 AIINLGNSTVIAPKMLMNLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP
 40 LLYMVVVSRRCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFCYDIAPLLALSCSDTYPE
 TTVFISAATNLFFSMITVLVSYFNIVLSILRIRSPGRKKAFSTCASHMIAVTVFYGTMLFMYLQP
 QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
 445).

45 ATGGCTCCTGAAAATTTACACCAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATTCCCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG
 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT
 TCCTGAGACATCTAGCTATCATCAATCTTGGCAACTCTACTGTCATTGCCCTAAAATGCTG
 ATGAACTTTTATGATAAAGAAAGAAACTACCTCATTCTATGAATGTGCCACCCAACTGGGAG
 50 GGTCTTGTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA
 TGTGGCCATTTGTAACCTCTGCTCTACATGGTGGTGGTGTCTCGCGGGCTCTGCCTCCTGC
 TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCACTTGTATATTC
 TCTGTGCTTATTGCTCTTCTAATATAATCAATCATTTTACTGTGATATTGCACCTCTGTT
 AGCATTATCTTGCTCTGATACTTACATACCAGAAACAATAGTCTTTATATCTGCAGCAACA
 55 AATTTGTTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTTGTCCATTCTA
 AGGATACGTTACACAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCTATGCTGAATCC
CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAT
CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

5

AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFFIFFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG
NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMQAIFLHFTGGAEMVLLVSMAYDRYVAIC
KPLHYMTLMSWQTCIRLVLASWVVGFBHSISQVAFVNLPCGPNEVDSFFCDLPLVIKLAACM
10 DTYVLGHMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLLFFGPCIFV
YVRPFSRFSVDKLLSVFYTIFTPLNPIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTGAGAAATTTGTGTTGCATGGACTCTGCACTTCAC
GACATCTTCAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT
15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCCTATGTACTT
CCTGCTGGGGAACCTAGCTTTCTGGACATGTGGCTGGCCTCATTTGCCACTCCCAAGATG
ATCAGGGATTTCCTTAGTGATCAAAAACCTCATCTCCTTTGGAGGATGTATGGCTCAAATCT
TCTTCTGCACTTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG
ATATGTGGCCATATGCAAACCCTTGCAATACATGACTTTGATGAGTTGGCAGACTTGCATC
20 AGGCTGGTGTGGCTTCATGGGTCGTTGGATTTGTGCACTCCATCAGTCAAGTGGCTTTCA
CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG
GTGATCAAACCTTGCCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG
GGTTGCTTTCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT
ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA
25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTGTATTATGTGCGGCCCTTCAGTAGGTTT
TCTGTGGACAAGCTGCTGTCTGTGTTTTATACCAATTTTACTCCACTCCTGAACCCCAATTAT
CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT
GACTTTTCAATGA (SEQ ID NO: 448).

30 **AOLFR240 sequences:**

MAGENHTTLEPFLLLGFSDLKALQGFLFWVLLVYLVTLGNLILLTQVSPALHSPMYFFLR
QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCQAQMYVFIVLGISECCLLTAMAYDRYVAIC
QPLRYSTLLSPRACLAMVGSSWLTGHTATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHR
SEISVMTATIVFIMPFSLIVTSYRILGAILAMASTQSRRKVFSTCSSHLLVVSLLFFGTASITYIRPQ
35 AGSSVTTDRVLSLFYTVITPMLNPIYTLRNDVRRALRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACTTGTCTGGG
40 TAACTCCCTGATCATCCTCCTCACACAGGTCAGCCCTGCCCTGCACTCCCCCATGTACTTCT
TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCCCT
GGCCAACTCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCAGATG
TACGTCTTCATTGTCTGGGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC
GATATGTTGCCATCTGCCAGCCCCCTACGCTATTCCACCCTCTTGAGCCACGGGCTGCTT
GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC
45 ATCTTCTCTACCTTTTCGAGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC
AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC
CATAGTCTTCATTATGATCCCTTCTCTCTGATTGTACCTCTTACATCCGCATCCTGGGTG
CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA
TCTGCTCGTGGTCTCTCTCTTTTGAACAGCCAGCATCACCTACATCCGGCCGAGGCA
50 GGCTCCTCTGTTACACAGACCGCGTCTCAGTCTCTTCTACACAGTCATCACCCCATGCT
CAACCCCATCATCTACACCCTTCGGAACAAGACGTGAGGAGGGCCCTGCGACACTTGGT
GAAGAGGCAGCGCCCCTCACCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

55 MPQILIFTYLNMFYFFPLQILAENLTMVTEFLLGFSSSLGEIQLALFVVFLFLYLVLSGNVTIIS
VIHLKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTLKIPSAEGRRKAFSTCAS
HLSVVIVHYGCASFYLRPTANYVSNKDRLVTVTYITVTPLLNPMVYSLRNKDVLAIKRVLG
KKGSLKLYN (SEQ ID NO: 451).

5
ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTTCCAGCCTTGGT
GAAATTCAGCTGGCCCTCTTTGTAGTTTTCTTTTTCTGTATCTAGTCATTCTTAGTGCGAA
10 TGTACCATATCAGTGTCTACCCACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTCC
TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCATTCTACCCAAGATGCTCATC
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT
CCTTGGTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTTATGATCGCTATGCTG
CCATTTGTCACCCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGGAAAACCTGGC
15 AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTTCAGCC
TCCCTTTTTGTAGCGCCAACAAAGTCAATCACTACTTCTGTGACATCTCAGCAGTCATTCTT
CTGGCTTGTACCAACACAGATGTTAACGAATTTGTGATATTCATTTGTGGAGTTCTTGTAC
TTGTGGTTCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG
ATTCCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTTG
TTATTGTTTCAATTATGGCTGTGCTTCTTACCTACCTGAGGCCTACAGCAAACCTATGTGTCC
20 AACAAAGACAGGCTGGTGACGGTGACATACACGATTGTCACTCCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTTGCTATCAGAAAAGTGTGGGCAAGAAA
GGTCTCTAAAACTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25 MNTTLFHPYSFLLLGIPGLESMHLVWGFPPFAVFLTAVLGNITLFIQTDSSLHHPMFYFLAILS
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY
TLVLTNKVVSVMALAIFLRPLVFVIPFVLFILRLPFCGHQIIPHTYGEHMGIA RLSCASIRVNIY
LCAISILVFDIIAIVISYVQILCAVFLSSH DARLKAFSTCGSHVCVMLTFYMPAFFSFMTHRFR
NIPHFHILLANFYVIPPALNSVYGVRTKQIRAQVLKMFFNK (SEQ ID NO: 453).

30
ATGAATACCACTCTATTTTCATCCTTACTCTTTCCTTCTTCTGGGAATTCCTGGGCTGGAAAG
TATGCATCTCTGGGTTGGTTTTCTTTCTTTGCTGTGTTCTGACAGCTGTCCTTGGGAATA
TCACCATCCTTTTTGTGATTGAGACTGACAGTAGTCTCCATCATCCCATTGTTCTACTTCTG
GCCATTCTGTCATCTATTGACCCGGGCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTTCATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCCCTCTTTGCTACACGTTGGTGCTGACAAACAAGGTGGTGTCAGTTATGGCA
CTGGCCATCTTTCTGAGACCCCTTAGTCTTTGTCATACCCCTTTGTTCTATTTATCCTAAGGCT
TCCATTTTGTGGACACCAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCCG
40 CTGTCTTGTGCCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT
CTTTGACATCATAGCAATTGTCATTTCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT
CTTCACATGATGCACGACTCAAGGCATTGACACCTGTGGCTCTCATGTGTGTGTCATGTT
GACTTTCTATATGCCTGCATTTTCTCATTGATGACCCATAGGTTTGGTCGGAATATACCTC
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA
45 ATTTATGGTGTCAGAAACAAACAGATTAGAGCACAAGTGCTGAAAATGTTTTTCAATAAAT
AA (SEQ ID NO: 454).

AOLFR243 sequences:

50 MEQVNKTVVREFVVLGFSSLARLQQLFVIFLLYLFTLGTNAIIISTIVLDRALHTPMYFFLAIL
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLLAAMGYDRYMAICNPLR
YSVLMGHGVCMGLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVLKASQHSQF
SQLVIFMLGVFALVIPLLLILVSYIRIISAILKIPSSVGRYKTFSTCASHLIVTVHYSCASFYLRPK
TNYTSSQD TLISVSYTILTPFNPMIYSLRNKEFKSALRRITIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
 CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCATTGTACCCAAGATGCTGG
 TTGACCTGCTGTCCAGAAGAAGACCATTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
 TTCTCTTTCTTTGGCTCCTCTCACTCCTTCTGCTGGCAGCCATGGGCTATGATCGCTATAT
 5 GGCCATCTGTAACCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACCTCCCTAGTATTTCA
 TCTGCCCTTCCACTCCTCCAACGAGCTCCATCACTTCTTCTGTGACATCTCCCTGTCTTA
 AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTCATGCTTGGTGTATTTGC
 CTTGGTCATTCTCTGCTACTTATCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA
 10 AAATCCCTTCCCTCCGTTGGAAGATACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG
 GTAAGTGTCACTACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC
 AAGCCAAGACACCCTAATATCTGTGTACATACCATCCTTACCCCATTTGTTCAATCCAATG
 ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAACT
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15

AOLFR244 sequences:

MWQEYYFLNVFFPLKVCCLTINSHVVILLPWECYHLIWKILPYIGTTVGSMEEYNTSSTDFTF
 MGLFNKRKETSGLIFAIISIFFTALMANGVMIFLIQTDLRHLTPMYFLLSHLSLIDMMYISRVPKM
 LVNYLLDQRTISFVGCTAQHFLYLTLVGAEFFLLGLMAYDRYVAJCNPLRYVLMSSRRVCMWL
 20 IAGSWFGGSLDGFLLTPITMSFPFCNSREINHFFCEAPVCLKACADTALYETVMYVCCVLMML
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSFLFYGAAMYTYMLPHSYHKPAQ
 DKVLSVFYTLTPMLNPLIYSLRNKDVTKALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC
 25 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT
 TACCTTATATCGGCACAAGTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
 CACTTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTGGCATCATCTCT
 ATCATCTTCTTACCGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT
 TGCGCCTTCATACACCCATGTAATTCCTCCTCAGCCACCTTTCCTTAATTGACATGATGTAT
 30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCCTT
 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCCTCTG
 CTGGGCCCTCATGGCCTATGACCGCTATGTGGCCATTTGCAACCCCTCTGAGATACCCGTGCC
 TCATGAGCCGCCGGGTCTGTTGGATGATTATAGCAGGTTCTGGTTTGGGGGCTCTTTGGA
 TGGCTTCTCTCTAACCCCATCACCATGAGCTTTCCTTCTGCAATTCCTGGGAGATTAACC
 35 ACTTCTTCTGTGAGGCACCAGCAGTCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA
 GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCTTCTCTGTAGTCCTTGCTT
 CCTATGCCCCGAATCCTGACTACAGTTCACTGTCATGAGCTCAGTGGAGGGCAGGAAGAAGG
 CATTTGCCACTTGCTCATCCCATGACTGTGGTGTCTTGTCTACGGGGCTGCCATGTAC
 ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCAGGACAAAGTCCTCTGTGTTTT
 40 ACACCATTCTCACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC
 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTGAGGAGGTGT
 CTTTGA (SEQ ID NO: 458).

AOLFR245 sequences:

45 MDLKNGLVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPLYFLLGN
 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLIIIMAFDRYVAICKP
 LHYRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNVINNIFCDLPLVIKLACIETYLE
 LFVIADSGLLSFTCFILLVSYIVILVSVPKSSHGLSKALSTLSAHIIIVTLFFGPCIFIYVWPFSLL
 ASNKTLAVFYTVITPLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

50

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGACGAT
 GGGAACTTCAAATTTCTTCTTTGTGACATTTCCCTGATCTACGGTGCTACTGTGATGGGA
 AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCCCTTCACTCTCCCTGTACTTTCT
 CTTGGAAATCTCTCTTTTTTGGACATGTGTCTCTCCACTGCCACAACACCCAAGATGATCA
 55 TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT
 CATGCACTTCTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
 TTTGCGATACTTTCATGGATAATTGGTTTTTACACTCCATAAGCCAGATAGTTTTAAACAAT
 GAACTTGCCCTTCTGTGGCCACAATGTCATAAAACAATATTTTGTGATCTTCCCCTTGTGA
 TCAAGCTTGCTTGCAATTGAAACATACACCCTGGAATTATTTGTGATTGCTGACAGCGGGCT
 5 GCTCTCTTTCACCTGTTTCATCCTCTTGCTTGTCTTACATTGTCATCCTGGTCAGTGTACC
 AAAAAATCATCACATGGGCTCTCCAAGGCGCTGCCACATTGTCTGCCCACATCATTGTG
 GTCACCTCTGTCTTGGACCTTGTATTTTATCTATGTTTGGCCATTCAAGTAGTTTGGCAAG
 CAATAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT
 10 CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLLGLPIRPEQQAFFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
 LALTDISFSSVTVPKMLMDMRTKYKSILYEECISQMYFFIFFTDLDSFLITSMAYDRYVAICHPL
 15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLLRLSFCAANTIPHVFCDLAALLKLSCDIFLNE
 LVMFTVGVVVITLPMFCILVSYGYIGATILRVPSTKGIHKALSTCGSHLSVVSLLYYGSIFGQYLF
 PTVSSSIDKDIVALMYTVVTPMLNPFYISLRNRDMKEALGKLFSRATFFSW (SEQ ID NO:
 461).

ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC
 CAGAGCAGCAGGCTGTGTTCTTACCCTGTTCTGGGCATGTACCTGACCACGGTGCTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTCACCTTCACACCCCCATGTAATTCT
 TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCATCTGTCATGTCCTAAGATGCTG
 ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT
 25 TTTTATAATTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGGATAT
 GTTGCCATATGTCACCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGCTTCTT
 AGTGGCTGTATCTTGGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC
 GGCTGTCTTTCTGTGCTGCGAACACCATCCCCATGTCTTCTGTGACCTTGCTGCCCTGCTC
 AAGCTGTCCCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTACAGTAGGGGTGGTGG
 30 TCATTACCCTGCCATTATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCATCCTG
 AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG
 TGGTGTCTCTTATTATGGGTCAATATTTGGCCAGTACCTTTTCCGACTGTAAGCAGTTCT
 ATTGACAAGGATGTCATTGTGGCTCTCATGTACACGGTGCTCACACCCATGTTGAACCCCT
 TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAACTCTTCAGTAGAG
 35 CAACATTTTCTCCTTGGTGACATCTGACTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGQHNLTVLTEFILMELTRRPELQIPLFGVFLVIYELITVVGNLTMILTKLDSHLHTPMYFSIRHL
 ASVDLGNSTVICPKVLANFVDRNTISYYACAAQLAFFLMFIIEFFILSAMAYDRYVAICNPLL
 40 YYVIMSQRLCHVLVGIQYLYSTFQALMFTIKFTLTFCGSNVISHFYCDDVPLLPMLCSNAQEIE
 LLSILFSVFNLISSFLIVLVSYMLILLAICQMHSAGEGRKKAFTSCGSHLTVVVVFYGSLLFMYMQ
 PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCTGATGGAACCTACAAGGCGGC
 CTGAGCTGCAGATTCCCCTTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC
 AACCTAACTATGATCATTTTGACCAAACCTGGACTCCCACTTACATACACCTATGTACTTTTC
 TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCATTTGTCCCAAGGTGCTGG
 CAAATTTTGTGTGGATCGAAATACTATTTCTATATGATGTGCTGCACAGCTGGCATTC
 TTCTTATGTTTATTATCAGTGAATTTTTCATCCTGTCAGCCATGGCCTATGACCGCTATGT
 50 GGCCATTTGTAACCCCTCTGCTCTATTATGTTATTATGTCTCAGCGACTGTGTCATGTACTGG
 TGGGCATTCAATATCTCTACAGCACATTTTCAGGCTCTGATGTTCACTATTAAGATTTTACA
 TTGACCTTCTGTGGCTCTAATGTATCATGCTATTTTACTGTGATGATGTTCTTGGCTACC
 TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAATT
 TGATCTCCTCTTCTGATAGTCTTAGTGTCTACATGTTGATTTTGTAGCTATATGTCAA
 55 ATGCATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTCCCATTGACAGTGG
 TGGTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATTCCACTCACTTCTTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPCALPTGGLLPHQHTMMELANVSSPEVFLVLLGFSTRPSLETVLFIIVLSFYMVLSILNGI
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWLG
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSSTLMLPLCG
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIARAVLKIRSAEGR
10 RKAFTNCSSHVAVVSLFYGSIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVKS
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
GATGAAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGCTCCTCTGGGCTTCTCCACACGA
15 CCCTCACTAGAACTGTCCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TTCTTGCCAACTCCCTTCTGGACATGAGCTTACCACGAGCATTGTCCACAGCTCCTG
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT
ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCTGCTGGCCACCATGTCCTATGACCGCT
20 ACGTGGCATCTGCAGGCCACTCCATTACACTGTCATTATGCATCCACAGCTTTGCCTTGG
GCTAGCTTTGGCCTCCTGGCTGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTGCGAGATGCCCTCA
TTATGCAACTGGCTTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT
TGCTTTGTGTGCTGCTCTGGGGCTCATCCTGGTCTCTTACGGCCACATTGCCCGGGCCG
25 TGTTGAAGATCAGGTCAGCAGAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCACG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG
AACCCTTATTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30 **AOLFR249 sequences:**

MKSQIEKSDLKYRAILLQKVTRMFLFWVLLVLSRLLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIIVLLIYVTSIGNIGMILLIKTDSRLQTPMYFFQHLAFVDICYTSAITPKMLQSFTEEN
NLITFRGCVIQLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQTVYIQLVAGSYIIGSI
35 NASVHTGFTFSLSFCKSNKINHFFCDGLPILALSCSNIDINIILDVVFVGFDMFTELVIIFSITYIM
VTILKMSSTAGRKKSFSSTCASHLTAVTIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGACTTAAAATATAGAGCCATTTTATTGCAAAAAGTC
40 ACAAGGATGTTCTGCTTTTCTGGGTCTTCTCTTGGTCCCTTCTAGACTTTTGGTAGTCAT
GGGTCGAGGAAACAGCACTGAAGTGACTGAATCCATCTTCTGGGATTTGGTGTCCAACAC
GAATTTACGCATGTCTTTTCATTGTACTTCTTCTTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTTC
CACAACATTTGGCTTTTGTGATATCTGTTATACCTTCTGCTATCACTCCCAAGATGCTCCAA
45 AGCTTCACAGAAGAAAATAATTTGATAACATTTTCGGGGCTGTGTGATACAATTCTTAGTTT
ATGCAACATTTGCAACCACTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACCTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTACATTTTCA
CTGTCCTTCTGCAAGTCTAATAAAATCAATCACTTTTTCTGTGATGGTCTCCCAATCTTGC
50 CTTTTCATGCTCCAACATTGACATCAACATCTTAGATGTTGTCTTTGTGGGATTTGACT
TGATGTTCACTGAGTTGGTCATCATCTTTTCTTACATCTACATTATGGTCACCACTGGAAG
ATGTCTTCTACTGCTGGGAGGAAAAAATCCTTCTCCACATGTGCTCCCACTGACAGCAG
TAACCATTTTCTATGGGACACTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAATATGAAAGTAGCCTCTATATTTTATGGCACTGTTATCCCATGTTGAATCCTTTAAT
55 CTATAGCTTGAGAAATAAGGAAGGAAAAATAA (SEQ ID NO: 468).

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV
 DMGLTSSVTTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY
 STVMRPQVCALMLALCWVLTNIVALTHTFLMARLSFCVTGEIAHFFCDITPVKLKSCSDTHINE
 5 MMVFLVGGTVLIVPFLCIVTSYIHVPAILRVTRGGVGKAFSTCSSHL CVV CVFYGT LFSAYLC
 PPSIASEEKDIAAAAMYTIVTPMLNPFYISLRNKDMKGALKRLFSHRSIVSS (SEQ ID NO: 469).

ATGGAAAACCAATCCAGCATTTCTGAATTTTTCTCCGAGGAATATCAGCGCCTCCAGAGC
 AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTG
 10 CTCATCATCTCGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTCTTGGC
 CAACCTGTCTTTTGTGACATGGGTTTAAACGTCCTCCACAGTTACCAAGATGCTGGTGAAT
 ATACAGACTCGGCATCACACCATCTCCTATACGGGTTGCCTCACGCAAATGTATTTCTTTCT
 GATGTTTGGTGATCTAGACAGCTTCTTCTGGCTGCCATGGCGTATGACCGCTATGTGGCC
 ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC
 15 ATTGTGCTGGGTCTCACC AATATCGTTGCCCTGACTCACACGTTCTCATGGCTCGGTTGT
 CCTTCTGTGTGACTGGGAAATTGCTCACTTTTCTGTGACATCACTCCTGTCCTGAAGCTG
 TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTTGTCTTGGGAGGCACCGTACTCA
 TCGTCCCTTTTTATGCATTGTCACTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC
 CGAACCCGTGGTGGGGTGGGCAAGGCCTTTCCACCTGCAGTTCACCTCTGCGTTGTTT
 20 GTGTGTTCTATGGGACCTCTTCAGTGCCTACCTGTGTCTCCTCCCTCCATTGCCTCTGAAGAG
 AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT
 ATAGCCTAAGGAACAAGGACATGAAGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA
 TTGTTTCTCTTAG (SEQ ID NO: 470).

AOLFR251 sequences:

MEGNKTWITDITLPRFQVGPAL EILL CGLFSAFYTLTLLGNVIFGII CLDCKLHTPMYFFLSHLA
 IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFHVECLILVMSYDRYADICHPLRY
 NILMSWRVCTVLAVASWVFSLLALVPLVLILRLPFCGPHEINHFCILSVLKLACADTWLNQV
 VIFAACVFILVGPLCLVLVSYLRLAAILRIQSGEGRRKAFSTCSSHL CVV GLFFGSAIVTYMAPK
 30 SRHP EEQKVL SLFYSLFNPMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA
 GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCTTCTATACTCACCTGCTGGGGAA
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC
 35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCA ACTATGTCCCAAGATGCTGACG
 AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT
 ATTTGGCTTTTGCTACGTAGAGTGTCTGATTTTGGTGGTGATGTCCTATGATCGCTATGCG
 GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGTCTGTG
 CTGTGGCTTCTCCTGGGTGTT CAGCTTCTCCTGGCTCTGGTCCCTTTAGTCTCATCCTGAGG
 40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT
 GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCATCTTGCAGCCTGCGTGTTTCATCCTG
 GTGGGGCCACTCTGCCTGGTGTGCTGCTCCTACTTGCGCATCCTGGCCGCCATCTTGAGGA
 TCCAGTCTGGGAGGGCCGAGAAAGGCCCTTCTCCACCTGCTCCTCCACCTTTGCGTGGT
 GGGACTCTTCTTTGGCAGCGCCATTGTACGTACATGGCCCCCAAGTCCCGCCATCCTGAG
 45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA
 TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG
 AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

MRLANQTLGGDFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL
 IDLTYISVTVPKMLVNQLAKDKTISVLGCGTQMYFYLQLGGAECCLLAAMAYDRYVAICHPLR
 YSVLMSHRVCLLLASGCWFVGSVDGFMLTPIAMSFPCRSH EIQHFFCEVPAVLKLS CSDTSLY
 KIFMYLCCVIMLLIPVTVISVSYYYIILTIHKMNSVEGRKKAFTTCSHITVVSIFYGAAIYNMYL
 PSSYQTPEKDMMSFFYTILTPVLNPIIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

55

ATGCGGCTGGCCAACCAGACCCTGGGTGGTGACTTTTTCCTGTTGGGAATCTTCAGCCAGA
 TCTCACACCCCTGGCCGCCTCTGCTTGTATCTTCAGTATATTTTGTATGGCTGTGCTTGG
 AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT
 TATAAACAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG
 5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCTTGGGTGTGGCACCCAGATGTAC
 TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT
 ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
 CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA
 TGAGCTTCCCTTCTGCAGATCCCATGAGATTGAGCACTTCTTCTGTGAGGTCCCTGCTGTT
 10 TTGAAGCTCTCTTGCTCAGACACCTCACTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
 CATGCTCCTGATACCTGTGACGGTCATTTCACTGTCTTACTACTATATCATCCTCACCATCC
 ATAAGATGAACTCAGTTGAGGGTCGAAAAAGGCCTTACCACCTGCTCCTCCACATTAC
 AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACTACATGCTCCCCAGCTCCTACCAA
 ACTCCTGAGAAAAGATATGATGTCATCCTTTTCTACACTATCCTTACACCTGTCTTGAATCC
 15 TATCATTTACAGTTTCAGGAATAAGGATGTCAACAAGGGCTTTGAAAAAATGCTGAGCGT
 GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

AOLFR253 sequences:

MTFSSSGNCEPVMCSGNQTSQNQTASTDFTLTGLFAESKHAALLYTVTFLLFLMALTNALL
 20 ILLIHSEPLHTPMYFFISQLALMDLMLYLCVTPKMLVGVQVTGDDTISPSGCGIQMFHLLTAG
 AEVFLLAAMAYDRYAAVCRPLHYPLLMNQRCVQLLVSAWVLMVMDGLLLTPITMSFFCQS
 RKILSFFCETPALLKLSCSDVSLYKMLTYLCCILMLLPIMVISSSYTLILHLHRMNSAAGRRKA
 LATCSSHMIIIVLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPVLNPLIYSLRNKDVTRAL
 RSMMQSRMNQEK (SEQ ID NO: 475).

25 ATGACTTTTTTTTCTCAGGGGGAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
 CTCAGAATCAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTTGCTGAGAGCAAGCA
 TGCTGCCCTCCTCTACACCGTGACCTTCCTTCTTTCTTGATGGCCCTCACTGGGAATGCCC
 TCCTCATCCTCCTCATCCACTCAGAGCCCCGCTCCACACCCCCATGTACTTCTTCATCAGC
 30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCAAAGATGCTTGTGGGCC
 AGGTCACTGGAGATGATAACATTTCCCCGTCAGGCTGTGGGATCCAGATGTTCTTCCACCT
 GACCTGGCTGGAGCTGAGGTTTTCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT
 GTTTCAGACCTCTCCATTACCCACTGCTGATGAACCAAGAGGGTGTGCCAGCTCCTGGTGT
 CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTACCCCCATTACCATGAGCTT
 35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC
 TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
 CTCACCCCCATCATGGTCATCTCCAGCTCATAACCCCTCATCCTGCATCTCATCCACAGGAT
 GAATTCTGCCGCCGGCCGAGGAAGGCCTTGGCCACCTGCTCCTCCCATGATCATAGTG
 CTGCTGCTCTCGGTGCTTCCTTCTACACCTACATGCTCCGGAGTTCTTACCACACAGCTGA
 40 GCAGGACATGATGGTGTCTGCCTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT
 ACAGTCTCCGCAACAAAGATGTCAACAGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
 ACCAAGAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

45 MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
 MDTLFICTTVPKLLADMVSKKISFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP
 VLMNRKKCLLLAAGAWFGGSLDGFLLPITMNPYCGSRINHHFCEIPAVLKLACADTSLEYET
 LMYICCVLMLLIPISIISTSYSLILLTIHRMPSAEGRRKAFTTCSHLTVVSIFYGAAFYTYVLPQS
 FHTPEQDKVVSAFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACSSAQKVATSDA (SEQ ID NO:
 50 477).

ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG
 CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGCCGTGACTGCAAAATTTGGT
 CATGATATCTTGATTCAGGTGGACTCTCGCCTCCACACCCCCATGTACTTTCTGCTCAGTC
 55 AGCTGTCCATCATGGACACCCTTTTCATCTGTACCACTGTCCCAAACTCCTGGCAGACAT
 GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
 CTGTAAACCCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGTCTTTTGCTGGCTGCT
 GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC
 CTTACTGTGGCTCCCGAAGTATCAACCATTTTTCTGTGAGATCCCAGCAGTTCTGAAACT
 5 GGCCTGTGCAGACACGTCCTTGTATGAAACTCTGATGTACATCTGCTGTGTCCTCATGTTG
 CTCATCCCCATCTCTATCATCTCCACTTCCTACTCCCTCATCTTGTTAACCATCCACCGCAT
 GCCCTCTGCTGAAGGTCGCAAAAAGGCCTTCACCACTTGTTCTCCCACTTGACTGTAGTT
 AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCTTCCACACCCCCG
 AGCAGGACAAAGTAGTGTACAGCCTTCTATACCATTGTCACGCCCATGCTTAATCCTCTCAT
 10 CTACAGCCTCAGAAACAAGGACGTCATAGGGGCATTTAAAAAGGTATTTGCATGTTGCTCA
 TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHDSRLHTPMYFLLSQLS
 15 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
 YPVLMSRKICWLIVAAAWLGGSIDGFLTPVTMQFPFCASREINHFFCEVPALLKLSCTDTSAY
 ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
 YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTF (SEQ
 ID NO: 479).

20 ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCAACG
 CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTGACCTCCATAGCCAGC
 AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTAATTCCT
 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCAAAAATGCTG
 25 GTCGACCAGGTGATGAGCCAGAGAGCCATTTCCTTTGCTGGATGCACTGCCAACACTCC
 TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCCTATGATCGCTAC
 GTAGCCATCTGCAACCCTCTGCACTATCCTGTCTCATGAGCCGCAAGATCTGCTGGTTGA
 TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTACCCCCGTCACCAT
 GCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC
 30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT
 GATGCTCCTCATCCCTTTCTCTGTCATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT
 ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG
 TGGTTGTCAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC
 ACCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC
 35 CACTCATTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA
 GGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

MGGKQPWWTEFILVGFQVGPALAILLCGLFSVFYTLTLLGNGVIFGHICLDSKLHTPMYFFLSHL
 40 AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVVMYSYDRYVAICHPF
 QYTVIMSWRVCTILASTCWIISFLMALVHTHILRPPFCGPQKINHFCQIMSVFKLACAGPRLNQ
 VVLYAGSAFIVEGPLCLELVSNLHILSRHLEDPMGRAADRLTLPAPSHLCMVGLLFGSTMVM
 YMAPKSRHPEEQKVLSLFYSLFNPMNLPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
 481).

45 ATGGGAGGCAAGCAGCCCTGGGTACAGAATTCATCCTGGTGGGATTCCAGGTTGGTCCA
 GCACTGGCGATTCTCCTCTGTGGACTCTTCTCTGTCTTCTATACACTCACCTGCTGGGGAA
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTAATTCCTCC
 TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
 50 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG
 TATTTGGCTTTTGTGTTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT
 GGCCATCTGCCACCCTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTCACGATCCTG
 GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG
 GCCGCTTTTGTGGCCCAAAAAGATCAACCACTTATCTGTCAAATCATGTCCGTATTCA
 55 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCTATATGCGGGTTCTGCGTTCAT
 CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTGCACATCCTGTCGCGCCATCTT

GAGGATCCAGTAATGGGGAGGGCCGACACCGACTTACTCTTCCTGCTCCTTCCCACCTTT
GCATGGTGGGACTCCTTTTTGGCAGCACCATGGTCATGTACATGGCCCCAAGTCCCGCCA
CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC
CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCTGAAAAGAGTGTGTGG
5 AACAGAGATCAAAGTGA (SEQ ID NO: 482).

AOLFR257 sequences:

MESNQTWITEVILLGFQVDPALELFLFGFFLLFYSLTLMGNGIILGLIYLD SRLHTPMYVFLSHL
AIVDMSYASSTVPKMLANLVMHKKVISFAPCILQTFLYLAFATECLILVMMCYDRYVAICHPL
10 QYTLIMNWRVCTVLA STCWIFSLLALVHTLILRLPFCGPQKINHFFCQIMSVFKLACADTRLN
QVVLFA GSAFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHLCVVGLFFGSAIVMYM
APKSSHSQERRKILSLFYSLFNPILNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA
15 GCTCTGGAGTTGTTCTCTTTGGGTTTTCTTGCTATTCTACAGCTTAACCTGATGGGAAA
TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC
CTGTCACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG
CAAATCTTGATGCACAAAAAGTCATCTCCTTTGCTCCTTG CATACTTCAGACTTTTTTG
TATTTGGCGTTTGCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG
20 TGGCAATCTGTCACCCCTTGCAATACACCCTCATTATGAACTGGAGAGTGTGCACTGTCTT
GGCTCAACTTGCTGGATATTTAGCTTTCTCTGGCTCTGGTCCATATTACTCTTATTCTGA
GGCTGCCTTTTGTGGCCACAAAAGATCAACCACTTTTCTGTCAAATCATGTCCGTATTC
AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCTTATTGCGGGTTCTGCGTTCA
TCTTAGTGGGGCCGCTCTGCCTGGTGCTGGTCTCCTACTTGCACATCCTGGTGGCCATCTTG
25 AGGATCCAGTCTGGGGAGGGCCGACAGAAAGGCCTTCTCTACCTGCTCCTCCCACCTCTGCG
TGGTGGGGCTTTTCTTTGGCAGCGCCATTGTCATGTACATGGCCCCCAAGTCAAGCCATTC
TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCTTTGAAA
CAGAGATCAATGTGA (SEQ ID NO: 484).

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AOLFR259 sequences:

MGDNQSRVTEFILVGFQLSVEMEVLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVVMYSYDRFVAICHPL
HYTVIMNWRVCTVLAITSWACGFSALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTWIN
35 EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKAFSTCSSHLCVVGLYFGMAMVVY
LVPDNSQRQKQKILTLFYSLFNPILNPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:
485).

ATGGGGGACAACCAATCACGGGTCACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG
40 GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAAA
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCAGACTGCGCACCCCATGTACTTCTTCC
TGTCACACTTGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA
AAACCTAGTGAAACACAAAAAACTATCTCGTTCATCTCTTGCAATTATGCAGATGGCCTTG
TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTTGT
45 GGCGATCTGCCATCCCCTGCATTACACTGTCATCATGAACTGGAGAGTGTGCACAGTACTG
GCTATTACTTCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG
GCTGCCCTTCTGTGGGGCCCAAGAGGTGAACCACTTCTCGGTGAAATTCTGTCTGTCTC
AAACTGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTCTTTGCTGGTGGTGTGTTG
TCTTAGTCGGGCCCCCTTCTTGATGCTGATCTCCTACATGCGCATCCTCTTGCCATCCTG
50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAGCCTTTTCCACCTGCTCCTCCCACCTCTGTG
TGTTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG
ACAGAAGCAGCAGAAAATTCTCACCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTATACAGAGCACTGCAGAAA
AAGAGGACCATGTGA (SEQ ID NO: 486).

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AOLFR24B sequences:

MPSINDTHFYPPFFLLGIPGLDTHLWISFPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
 LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFHMFMTGMETVLLVVMAYDRFVAICNP
 LQYTMILTNKTISILASVVVGRNLVLVTPFVFLRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN
 5 IYGLMVISYIIVDVILIASSYVLILRAVFRLP SQD VRLKAFNTCGSHVCVMLCFYTPAFFSFMTH
 RFGQNIPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCTTCTTCTCCTGCTAGGAATACCAGG
 ACTGGACACTTTACATATCTGGATTTCTTTCCCATTTCTGTATTGTGTACCTGATTGCCATTG
 10 TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATGTT
 CTACTTCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA
 TGCTAGGAATCTTCTGGTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT
 GTTCTTTATTACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTGCATGGCTTATGACC
 GCTTTGTTGCCATCTGCAACCTCTCCAGTACACCATGATCCTCACCATAAAAACCATCAG
 15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAAACCCATTTGTGTTTCTCA
 TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
 TCTGGCCGGGTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
 TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCTATGTGCTTATCCTTAGAGCTGT
 TTTTCGCCTTCCCTCTCAAGATGTCCGACTAAAGGCCTCAATACCTGTGGTTCTCATGTCT
 20 GTGTTATGCTGTGCTTTTACACACCAGCATTTTCTTTTCTTTATGACACATCGTTTGGCCAA
 AACATTCCCCACTATATCCATATCTTTGGCTAACCTGTATGTGGTTGTTCCCACTGCCCT
 TAACCTGTCAATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT
 GTACAGAAAGAATAA (SEQ ID NO: 488)

AOLFR33B sequences:

MLHTNNTQFHPSTFLVVGVPGLDVHVWIGFPFFAVYLTALLGNIIILFVIQTEQSLHQPMFYFL
 AMLAGTDLGLSTATIPKMLGIFWFNLGEIAGACITQMYTIHICTGLESVVLTVTGIDRYIAICNP
 LRYSMILTNKVIALGIVIVRTL VFVTPFTFLTLRLPFCGVRIIPHTYCEHMG LAKLACASINVIY
 GLIAFSVGYIDISVIGFSYVQILRAVFHLP AW DARL KALSTCGSHVCVMLAFYLPALFSFMTHRF
 30 GHNIPHYIHILLANLYVVFPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ
 (SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCACCCTTCCACCTTCTCGTAGTGGGGGTCCCAG
 GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT
 35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
 TTTTACTTCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA
 AGATGCTGGGAATTTTCTGGTTAATCTTGGAGAGATTGCATTTGGTGCCTGCATCACACA
 GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
 GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
 40 TAGCCATTCTGGGCATAGTCATCATTGTCAGGACTTTGGTATTTGTGACTCCATTACATTT
 CTCACCCTGAGATTGCCTTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT
 GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA
 GTGGGATACATTGACATTTCTGTGATTGGATTTTCTATGTCCAGATCCTCCGAGCTGTCTT
 CCATCTCCCAGCCTGGGATGCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGCTGTGT
 45 GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTTCTTTCATGACACACCGCTTTGGCCACAA
 CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTCCCCCTGCTCTTA
 ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA
 ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTCAGTTAGACA
 ATAA (SEQ ID NO: 490)

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AOLFR112B sequences:

MKNKTVLTFBLLGLTDVPELQVAVFTFLFLAYLLSILGNLTILTLTLDLHLQTPMYFFLRNFSF
 LEISFTNIFRVLISITTNKKSISFAGCFTQYFFAMFLGATEFYLLAAMS YDRYVAICKPLHYTTI
 MSSRICIQLIFCSWLGLMAIPTITLMSQQDFCASNRLNHYFCDYEP LLELSCSDTSLIEKV VFL
 55 VASVTLVVTLLVLSYAFIHK TILKLPSAQQR TKAFSTCSSHMIVISLSYGSCMFMYINPSAKEG
 DTFNKGVALLITSVAPLLNPFITYTLRNQVQKQPFKDMVKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC
 TCCAGGTGGCAGTTTTACCTTTCTTTTCTTGCGTATTTACTCAGCATCCTTGGAATCTG
 ACTATCCTCATCCTCACCTTGCTGGACTCCCACCTTCAGACTCCCATGTATTTCTTTCTCCG
 5 GAACTTCTCCTTCTTGGAATTTCCCTTCACAAACATCTTCATTCCAAGGGTCTGATTAGCA
 TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT
 GTTCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC
 ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT
 TCTGCTCTTGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA
 10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA
 CTCTCATGTTGAGACACAAGCCTCATAGAGAAGGTTGTCTTCTTGTGGCATCTGTGACCC
 TGGTGGTCACTCTGGTGCTAGTGATTCTCTCCTATGCATTCAATTATCAAGACTATTCTGAAG
 CTCCCTCTGCCCAACAAAGGACAAAAGCCTTTTCCACATGTTCTTCCACATGATTGTCAT
 CTCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT
 15 ACATTCAACAAGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT
 TTACCCCTAAGGAACCAACAGGTAAAACAACCCTTCAAGGATATGGTCAAAAAGCTTCT
 GAATCTTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQTAPSEFILGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL
 ALIDICYTTTNVPQMMVHLLSEKKIISYGGCVTQLFAFIFFVGSECLLLAAMA YDRYIAICKPLR
 YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFLHLPFCGNNQINYYFFCDIPLLILSCGDTSLNE
 LALLSIGILISWTPFLCIISYLYIISTILRIRSSEGRHKAFSTCASHLLIVILYYGSAIFTYVRPISSYS
 LEKDRLISVLYSVVTPLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA
 ATGAATTGCAGTATTTACTCTTACCATCTTCTTTCTGACCTACATATGCACCTTAGGAGGC
 AATGTTTTTATCATTGTGGTGACCATAGCTGATTCCCACCTACACACACCCATGTATTATTT
 CCTAGGAAATCTTGCCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG
 30 GTGCATCTTCTGTGAGAGAAGAAAATCATTTCTATGGAGGCTGTGTGACCCAGCTCTTTG
 CATTCATTTTCTTTGTTGGCTCAGAGTGCTCCTCCTGGCAGCAATGGCATATGATCGATAT
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACAAGGCCCTGTGCAGCTGGT
 TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT
 CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC
 35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACTGGCTTTGCTGTCCATTGGGATCCTC
 ATAAGCTGGACTCCTTTCTGTGCATCATCTTTCTACCTTTACATCATCTCCACCATCCT
 GAGGATCCGTTCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCACCTGCTC
 ATTGTTATTCTCTATTATGGCAGTGCTATCTTACCGTATGTGAGGCCCATCTCATCTTACTC
 TCTAGAGAAAAGATAGATTGATCTCAGTGCTGTATAGTGTTGTACACCCATGCTGAATCCT
 40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG
 TGGCAGCCACCAGTTTTCTTCTTGATATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

45 MARKDMAHINCTQATEFILVGLTDHQELKMPLFVLFSLIYLFVVGNLGLILLIRADTSINTPM
 YFFLSNLAFVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLLASMAYDRY
 VAICNPLLYMVVMTPGICQLVAVPYSYSFLMALFHTLTFRLSYCHSNIVNHFYCDDMPLRL
 TCSDTRFKQLWIFACAGIMFISSLLIVFVSYMFISAILRMHSAEGRQKAFSTCGSHMLAVTIFYG
 TLIFMYLQPSSSHLDTDKMASVFYTVIIPMLNPLIYSLQNKKEVKEALKKIINKN (SEQ ID NO:
 495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG
 GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC
 TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA
 CACCAATGTACTTCTTTCTTAGCAACCTAGCTTTTGTGGATTTCTGTTACTCTTCTGTCATT
 55 ACACCCAAAATGCTTGGGAATTTCTGTACAAACAAAATGTTATATCCTTTGATGCATGTG
 CTACTCAACTGGGCTGCTTTCTACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTAC
 ACCATCCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCATTCTATTGTGA
 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT
 5 GCCTGTGCTGGTATCATGTTTCATTTCCCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTCATC
 ATTTCTGCCATCCTGAGGATGCATTAGCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTTATGTACTTACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATT
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 10 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

MAEVNIIVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL
 AFVDLCYSSAITPKMMVNFVVERNTIPFHACATQLGCFLTFMITECFLLASMA YDCYVAICSP
 15 HYSTLMSRRVCIQLVAVPYIYSFLVALFHTVITFRLTYCGPNLINHFYCDLPLALSCSDTHMK
 EILIFAFAGFDMISSSIVLTSYIFILAILRIRSTQGQHKAI STCGSHMVTVTIFYGTLIFMYLQPKS
 NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILFLKIRKLY (SEQ
 ID NO: 497)

ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCTGAAAGGAATTACCAACCGGC
 CAGAGCTTCAGGCCCGTGCTTTGGGGTGTITTTAGTTATCTATCTGGTCACAGTGCTGGG
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTAAT
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG
 GTGAATTTTGTGTGGAAACGCAACACCATTCCCTTTCCATGCTTGTGCAACCCAACTGGGTT
 25 GTTTTCTCACCTTCATGATCACTGAGTGTTTCCCTTCTAGCCTCCATGGCCTACGATTGCTAT
 GTCGCCATCTGTAGTCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC
 TGGTGGCAGTTCCATATATATACAGCTTCCCTGGTTGCCCTCTTCCACACCGTTATCACTTTC
 CGTCTGACTTACTGTGGCCCAAACCTTAATTAACCATTCTATTGTGATGACCTCCCTTCTT
 AGCTCTGTCTGCTCAGACACACATGAAGGAAATCTGATATTTGCCCTTGGCTGGCTTT
 30 GATATGATCTCTTCCCTCTTCCATTGTCCTCACCTCCTACATCTTTATTATTGCCGCTATCCTA
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCCACCTGTGGCTCCCATGATGGTA
 CTGTCACTATTTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAACTCACTCC
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG
 35 GTTGTGAAAACCTACAGATATTAACATTTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:
 498)

AOLFR225B sequences:

MKNRTMFGEFILLGLTNQPELQVMIFIFLFLTYMLSILGNLTITLTLLDPHLQTPMYFFLRNFSF
 40 LEISFTSIFIPRFLTSMITGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLELMVI
 LLAVVTLMTLVLTLSYTYIIRTLRIPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKE
 GGA FNKGIAVLITSVTPLLNPFITYTLRNQVQKQAFKDSVKKIVKL (SEQ ID NO: 499)

ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC
 TCCAAGTGATGATATTCATCTTTCTGTTCCCTCACCTACATGCTAAGTATCCTAGGAAATCTG
 ACTATTATCACCCCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCCCTCCG
 GAATTTCTCCTTCTTAGAAATTTCTTACATCCATTTTATTCCCAGATTTCTGACCAGCA
 TGACAACAGGAAATAAAGTTATCAGCTTTGTCTGGCTGCTTGACTCAGTATTTTTTGCTAT
 50 ATTTCTTGGAGCTACCGAGTTTACCTCTTGGCCTCCATGTCTTATGATCGTTATGTGGCCA
 TCTGCAAAACCCTTGCAATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACTAGTGTT
 CTGCTCCTGGTTGGGGGATTCTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCT
 TGCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC
 55 ATGGTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA
 TCCCTTCTGCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTTCCCTCCCATGATTGTCATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG
CTTTCAACAAAGGAATAGCTGTACTCATTCTCGTTACTCCCTTACTGAATCCCTTCATA
TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTCAAGGACTCAGTCAAAAAGATTGTG
AAACTTTAA (SEQ ID NO: 500)

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AOLFR274B sequences:

MEFVFLAYPSCPELHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV
VVPFILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLMLTL
CVHLVVASVISGLFSLQLVAFIFSLPFCQAQIEHFFCDVPPVMHVCAQSHIEQSVLVAAIL
AIAVPFFLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVVLLQYGCCAFMYLCPSSSYNPKQ
DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

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ATGGAATTTGTGTTCCCTGGCCTATCCCTCCTGCCAGAACTGCATATTCTGTCCTTCCTTGG
GGTCAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTAC
ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGGGCAGCCTTTCTGGGATTGAAA
TATGCTACACTGCAGTGGTGGTGCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC
CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGCTGAT
TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTTGCCACCCGTTGCAGTA
CCCTCTCCTCATGACATTGACTCTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC
TGTTCTGTCTTACAACTGGTGGCCTTCATCTTCTCTGCCATTCTGCCAGGCTCAGGGC
ATTGAGCACTTCTTTGTGATGTGCCACCAGTCATGCATGTTGTTGTGCTCAGAGTCACAT
TCATGAGCAGTCAGTGTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC
ACCACTCTTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC
ACCGGGCCTTCTCCACCTGCTCTTCCACCTCACTGTGGTGTGCTGCAGTATGGCTGCTGT
GCCTTCATGTACCTGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC
TGGTGTACACATTGGGAACCCCACTGCTCAACCCCACTTATCTATGCCCTGAGGAACAGTGA
GATGAAAGGGGCCGTAGGGAGAGTTCTTACCAGGAAGTGCCTTTCCAGAACAGCTAG
(SEQ ID NO: 502)

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AOLFR276B sequences:

MGGFGTNISSTTSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIKEEQSLHQPMMYFLS
LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFHDHYVAICNP
LRYATVLTDRVAHNGISIVRSFCMVFLPFLKRLPFCKASVVLAAHSYCLHADLIRLPWGDT
TINSMYGLFIVISAFGVDSLILLSYVLILHSVLAIASRGERLKTNTCVSHIYAVLIFYVPMVSVS
MVHRFGRHAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

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ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG
AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCTT
CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGCAACAGCCAATG
TACTACTTCTGTCTCTTTTCTGTTAATGACCTGGGTGTGCTCTTTCTACATTGCCCACT
GTACTGGCTGTGTGTGTTTTCATGCCAGAGACAACTTTTGATGCCTGCCTGGCCGAGA
TGTTCTTCATCCACTTTTCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTGTGAC
CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG
CCCAACATGGCATATCCATTGTCTATCCGAGCTTCTGCATGGTATTCCCACTTCCCTTCCTC
CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCATTCCTACTGTCTGCATG
CAGACCTGATTGCGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTTCAT
TGTCATCTCTGCCTTTGGTGTAGATTCACTGCTCATCCTCCTCTCCTATGTGCTCATTCTAC
ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC
ACATATCTATGCAGTGCTGATCTTCTATGTGCTATGGTTAGTGTGCTCATGGTTCATCGAT
TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTTCATGTCTCTTTGTACCTCCAATGCTCT
ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

AOLFR311B sequences:

MDWENCSSLTDFLLGITNNPEMKVTLFAVFLAVYIINFANLGMIVLIRMDYQLHTPMYFFLS
HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLSVMAFDYKAIINP
LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPLLLLSRSDTQV

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NELVLFTVFGFIELSTISGVFISYCYIILSVLEIHS A EGRFKALSTCTSHLSA V AIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTATTTTCTCTTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTTATATCATTAAATTTCTCAGCAA
ATCTTGGAATGATAGTTTAAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCAAGATGCTGG
TAGATCTACTTGCCAAGAACAAGTCAATACCCCTTCTATGGCTGTGCTCTGCAATCTTGGT
10 CTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTGCTGATGGCCCTTGATCGGTACA
AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTATTACCGTCTTTGGTTTAA
TTGAACGAGTACCATTTACAGGAGTTTTCATTTCTTATTGTTATATCATCCTATCAGTCTTG
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTACATGCACCTCCCACTTATCTG
CGGTTGCAATTTTCCAGGGAAGTCTGCTCTTTATGTATTTCCGGCCAAGTCTTCCTATTCT
CTAGATCAAGATAAAATGACCTCATTGTTTTACACCCCTGTGGTTCCCATGTTGAACCCCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAACTGAAAAATAAAAT
TTATTTTAA (SEQ ID NO: 506)

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AOLFR314 sequences:

MEVKNCCMVTEFILLGIPHTGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFHFLGSIECFLFTVMAYDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCIHSSILSLTFTLPYCGPNEVDHFFCDIPALLPLACADTSL
25 AQRVSFTNVGLISLVCFLILLSYTRITISILSIRTTEGRRRAFSTCSAHLIALCAYGPIITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCACACACA
GAGGGGCTGGAGATGACACTTTTTGTCTTATTCTTGCCCTTCTATGCCTGCACTCTACTGGG
30 AAATGTGTCTATCCTTGTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT
TCCTGGGAAACTTGTCTGTGTTGACATGGGTTTCTCCTCAGTGACTTGTCCAAAATGCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTCT
TCTTCCATTTCTCGGGAGCATTGAGTGCTTCTGTTTACGGTGATGGCCTATGACCGCTTC
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCATTCAATCCAGTATCTTGACCTCCCTCACCTTC
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTTAGCCAGAGGGTGAGCTTCACCAACGTTGGCCTC
ATATCTCTGTGCTTTCTGCTAATTTCTTTATCCTACACTAGAATCACAATATCTATCTT
AAGCATTCGTACAAGTGGGGCCGTCGCCGTGCCTTCTCCACCTGCAGTGCTCACCTCATT
40 GCCATCCTCTGTGCCTATGGGCCCATCATCACTGTCTACCTGCAGCCACACCCAACCCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAAACAATATTGCACAGGACAGG
CCATGTTCTCTGAGAGTTAG (SEQ ID NO: 508)

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AOLFR324B sequences:

MPIANDTQFHTSSFLLLGIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVIQTEQSLHEPMYCLA
MLDSIDLSLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFFTVMESIVLVAMAFDRYIAICKPL
WYTMILTSKIISLIAGI AVLRSLYMVIPLVFLRLPFCGHRIPHTYCEHMGIA RLACASIKV NIM
FGLGSISL LLLDVLLI LSHIRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
50 DIPQYIHFILANLYVVVPPTLNPVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCATACTTCTTCATTCCCTACTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC
TGGGAAATGCTGCTATCTTCTTGTGATCCAAACTGAGCAGAGTCTCCATGAGCCCATGTA
55 CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTCCTCAA
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTGGAGGCTACCTTTCTCAGA

TGTTCCTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
 CGCTACATTGCCATTTGCAAACCTCTTTGGGTACACCATGATCCTCACCAGCAAAATCATCA
 GCCTCATTGCAGGCATTGCTGTCCTGAGGAGCTTGTACATGGTCATTCCACTGGTGTCTCT
 CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
 5 GCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
 TTCTCTCTTGTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT
 CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT
 GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTTCTTTACACACTGCTTTGGCCAT
 10 GATATTCCTCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCTCCACCCT
 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC
 TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

15 MALGNHSTITEFLLGLSADPNIRALLFVLFLGIYLLTIMENLMLLLVRADSCLHKPMYFFLSH
 LSFVDLCFSSVIVPKMLENLLSQRKTIISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAAIRRP
 LLYGQIMGKQLYMHVWGSWGLGFLDALINVLLAVNMVFCBAKIIHHYSYEMPSLLPLSCSDI
 SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
 MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC
 CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTTGGGGATTACCTCCTGACCATAATGGA
 AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT
 TCCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTTCAAGTCATTGTGCCCAAGATGCTG
 GAGAACCTCCTGTACAGAGGAAAACCATTTTCAGTAGAGGGCTGCCTGGCTCAGGTCTTCT
 25 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA
 TGCTGCCATCCGCCGCCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC
 CTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCTCCTAGCTG
 TAAACATGGTCTTTTGTGAAGCAAAATCATTACCACTACAGCTATGAGATGCCATCCCT
 CCTCCCTCTGTCCTGCTCTGATATCTCCAGAAGCCTCATCGTTTGTCTGCTCCACTCTCC
 30 TACATGGGCTGGGAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC
 CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCACCTCA
 CTGCAGTGACACTTTACTATGGCTCAGGTTTGTCTCGCCATCTCATGCCAACTCAGGTTC
 CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCTCA
 TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAAGAACTTTGAAAAATATT
 35 TGCAATATACCAGACGTTGA (SEQ ID NO: 512)

Claims:

1. A method for representing sensory perception of one or more odorants comprising:
 - 5 (a) providing a representative class of n olfactory receptors or ligand-binding domains thereof;
 - (b) measuring values X_1 to X_n representative of at least one activity of the one or more odorants selected from the group consisting of binding of the one or more odorants to the ligand-binding domain of at least one of the n
 - 10 olfactory receptors, activating at least one of the n olfactory receptors with the one or more odorants, and blocking at least one of the n olfactory receptors with the one or more odorants; and
 - (c) generating a representation of sensory perception from the values X_1 to X_n ;
- 15 wherein at least one of the n olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133,
 - 20 SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169,
 - 25
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SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID
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SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID
NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205,
5 SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID
NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223,
SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID
NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241,
SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID
10 NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259,
SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID
NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277,
SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID
NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295,
15 SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID
NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313,
SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID
NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331,
SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID
20 NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349,
SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID
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25 SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID
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NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421,
SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID
30 NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439,
SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID
NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457,
SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID

NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475,
SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID
NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493,
SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID
5 NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:
511.

2. The method of Claim 1, wherein at least one of the olfactory receptors
specifically recognizes the odorant, and there are between 5 and 350 of the n olfactory
10 receptors selected from the listed amino acid sequences.

3. The method of Claim 1, wherein at least two different activities are measured
to provide the values X_1 to X_n .

15 4. The method of Claim 1, wherein each odorant receptor is expressed in cells,
and the cells expressing each odorant receptor are located at an identifiable position.

5. The method of Claim 1, wherein at least one olfactory receptor is soluble, and
binding of odorant to a ligand-binding domain of the soluble olfactory receptor is
20 measured in solution.

6. The method of Claim 1, wherein at least one olfactory receptor is in solid state,
and binding of odorant to a ligand-binding domain of the solid-state olfactory receptor
is measured on a substrate.

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7. The method of Claim 1, wherein the value measured for binding is above a
preset limit for specific binding to olfactory receptors.

8. The method of Claim 1, wherein the value measured for activating an olfactory
30 receptor is derived from a signal selected from the group consisting of intracellular
 Ca^{2+} , cAMP, cGMP and IP3.

9. The method of Claim 1, wherein the value measured for activating an olfactory receptor is above a preset limit for specific activation.
10. The method of Claim 1, wherein the value measured for blocking an olfactory
5 receptor is at least a reduction in binding of the odorant or activation by the odorant.
11. The method of Claim 1, wherein the representation of sensory perception is generated with a neural network.
- 10 12. A biosensor comprised of the n ligand-binding domains or olfactory receptors of Claim 1.
13. A method for producing a database of odorant representations comprising:
15 (a) providing one or more known odorants and
(b) generating a representation of the one or more known odorants in accordance with the method of Claim 1 to produce the database.
14. A database produced by Claim 13.
- 20 15. A method of identifying an unknown odorant comprising:
(a) measuring values X_1 to X_n representative of at least one activity selected from the group consisting of binding the unknown odorant to a ligand-binding domain of at least one of n olfactory receptors, activating at least one of n olfactory receptors with the unknown odorant, and blocking at
25 least one of n olfactory receptors with the unknown odorant;
(b) generating a representation of the unknown odorant from the values X_1 to X_n ; and
(c) comparing the unknown odorant's representation to the database of Claim 14 to identify the known odorant which is most similar in
30 representation.
16. A method of producing an artificial odorant comprising:

- 5 (a) measuring values X_1 to X_n representative of at least one activity selected from the group consisting of binding a desirable odorant to a ligand-binding domain of at least one of n olfactory receptors, activating at least one of n olfactory receptors with a desirable odorant, and blocking at least one of n olfactory receptors with a desirable odorant;
- (b) generating a representation of the desirable odorant from the values X_1 to X_n ;
- 10 (c) decomposing the desirable odorant's representation into representations of known odorants from the database of Claim 14 or superposing known odorants' representations from the database to reproduce the desirable odorant; and
- (d) formulating the known odorants to reproduce sensory perception of the desirable odorant and thereby produce the artificial odorant.

15 17. An artificial odorant produced by Claim 16.

18. A method of identifying a primary odorant related to sensory perception comprising:

- 20 (a) providing a representative class of n olfactory receptors or ligand-binding domains thereof,
- (b) measuring at least one activity of a odorant selected from the group consisting of binding of the candidate odorant to the ligand-binding domain of at least one of the n olfactory receptors and activating with the candidate odorant at least one of the n olfactory receptors, and
- 25 (c) identifying the candidate odorant as a primary odorant if only one or less than 10% of the representative class of n olfactory receptors is bound or activated;

wherein at least one of the n olfactory receptors has an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID

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NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID
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5 NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID
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 NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:
 511.

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19. A primary odorant identified by Claim 18.

20. A method of identifying a compound which blocks activation by a odorant of
 at least one olfactory receptor comprising:

- 25 (a) producing a structurally-related candidate compound from a ligand of
 the at least one olfactory receptor,
 (b) measuring activation by the odorant of the at least one olfactory
 receptor with the candidate compound, and
 (c) identifying the candidate compound as a compound which blocks
 30 activation if activation of the at least one olfactory receptor is reduced or
 inhibited;

wherein at least one of the olfactory receptors has an amino acid sequence selected
 from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID

NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID
NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID
NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID
NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID
5 NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID
NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID
NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID
NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID
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30 SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID
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5 SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID
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25 21. The method of Claim 20, wherein the ligand is a primary odorant.

22. A compound which blocks activation of an olfactory receptor identified by Claim 20.